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Copyright (c) 1993 - 2000 Compugen Ltd
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ACCESSION VERSION KEYWORDS SOURCE RESULT 1
BE168072/c
LOCUS
DEFINITION COMMENT REFERENCE JOURNAL TITLE AUTHORS ORGANISM MEDLINE Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2=QV3-HT0513-150
300-117-f106t3=2000-03-154t4=1)
Seq primer: puc 18 forward Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and BE168072 569 bp mF QV3-H70513-150300-117-f10 BE168072 BE168072.1 GI:8630793 EST. Simpson, $A,\,J\,.$ Shotgun sequencing of the human transcriptome with ORF expressed Tel: +55-11-2704922 Fax: +55-11-2707001 20202663 sequence tags Eukaryota; Metazoa; Mammalia; Eutheria; Homo sapiens (bases Natl. Acad. 1 to 569) Sci. U.S.A. Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo. HT0513 Homo sapiens cDNA, mRNA sequence 97 (7), 3491-3496 (2000) 01509-010, Sao Paulo-SP, 21-JUN-2000

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Sus scrofa
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306720 MARC
BG385110
BG385110.1
EST.
                                                          Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with
v0.980904.e. Vector identified by cross_match with the -mi
                                                                                                                USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
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Contact: Smith TPL
                                                                                                                                                                                                                                                       Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennet and Keele, J.W.
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/dev_stage="Adult"
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                                                            Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 837)

28 NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

10 (Dabsed (1999)

11 (Dabsed (1999)

12 (Contact: Robert Strausberg, Ph.D.

13 Email: cgapbs-r@mail.nih.gov

14 Tissue Procurement: Dr. Daniel McVicar, DBS/NCI

15 CDNA Library Preparation: Ling Hong/Rubin Laboratory

16 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

17 DNA Sequencing by: Incyte Genomics, Inc.

18 Clone distribution: MGC clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                                                           BG743866 837 bp
602722621F1 NIH_MGC_106
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Seq pri
                http://image.llnl.gov
Plate: LLCM1688 row: i column: 05
                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
High quality sequence stop: 807
                                                                                                                                                                                                                                                                                                                             BG743866.1
                                                                                                                                                                                                                                                                                                                                             BG743866
                                                found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="pooled"
/lab_host="Upling"
/note="Vector: pcMV SPORT6; Site_1: XbaI;
Library made from pooled tissue from day 1
and 30 embryos."
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/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
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                                                                                                                                                                                                                                                                                                                             GI:14054519
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Pred. No. 4.1e-46;
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GGACCTTGGCTTGCGTTGCGGTCATCTTCTCCCTGCTGCTCGTGGTGGTCCGGAC

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1434 gecetatggtgtggeagtggggtgteecetecetecetegtegtggtettecegae
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                                                                                                                                                                                                                                                                                                                                   catgctggtcctggggatctatctgtatcctctccctaagtctgtgctaggagccctgat 1313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | gcacggctacgacgtggattcgaaccaggagatgatcgctctcggctgcagcaacttctt 1133
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                                                                                  CAATCGGGCGGATCTGCTTATCTGGCTGGTGACCTT - CACGGCACCATCTTGCTGAACCT
                                                                                                             gagcaagctggactgttgcatctgggtagtgagcttcctctcctcctccttcttcctcagcct
                                                                                                                                                                                       CATTGTGAACCTGAAGGCATGCTGAGGCAGCTCAGCGACATGCGCTCCCTCTGGAAGGC
                                                                                                                                                                                                                                                                                             CATTGTCAAACTTGGGGAACTCTTCCATGACCTGCCCAAGGCGGTCCTGGCAGCCATCAT
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4849228"
/clone="IMAGE:4849228"
/clone=lib="NIH_MGC_106"
/tissue_type="natural killer cells, cell line"
/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5; adaptor:
into EcoRI/XhoI sites using the following 5; adaptor:
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Pred. No. 6.8e-31;
0; Mismatches 360;
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ttggctccttctttaaaattcatgtcatttgctgtgcgctttc-tgtcactctggctgtg 1191
                                                                                                                                                                                                                                                                                               AGCACGGCTACGACGTGGAGTCGAACCAGGAGATGATCGCTCTCGGCTGCAGCAACTTCT 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CMl&t2=CMl-ET0042-
130600-264-h04&t3=2000-06-13&t4=1)
Seq primer: puc 18 forward
Title Company of the primer of the pure of the pur
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
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Ludwig Institute for Cancer Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer cesearch. 10 (11), 1757-1771 (2000)
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome research. 10 (10), 1617-1630 (2000)
  Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
                                                                         Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute Physical and Chemical Research (RIKEN), Laboratory for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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RIKEN Genome Exploration Research Group Phase II Team and the
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Japan (E-mail:genome-res@gsc.riken.go.jp,
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                                                                                                                                               {\tt GGGCACATCTAGACACATATCTGTGGGTCCATTTCCAGTTCTGAGTATGATGGTGGGAGT}
-AGCTCCACAGAAAATGACTCGTTCATAGAGGAGAAAGTAATGGTGGCTGCATCAGTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     end: BamHI. Host: DH10B
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/protein_id="BaB31279.1"
/protein_id="BaB31279.1"
/protein_id="BaB334"
/db_xref="rd::12858334"
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LGVLQVGFVVITLSESLISGFTTAAAHIVLVSQLKFMLQLPVPAYSDPFSIFKVLESV
FTQIQKTNIADLVTSVIILVVVFVFKEINQRYRSKLPVPIPIELIMVLIVIRRLSLTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="colon"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
239. .1069
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/strain="C57BL/6J"
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/db_xref="MGD:MGI:1918793"
/clone="9030623B18"
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2M0116E10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0116E10 F, DNA sequence.
AZ833796
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                                                                                                                                                                                                                                                                                                                                                                                  Tel:
                                                                                                                                                                                                                                                                        Seq primer: CGTTGTAAAAACGACGGCCAGTClass: plasmid ends
                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0116 row: E column: 1
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University of Utah
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GSS.
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                                 /note="Vector: PWD42nv; Purified genomic DNA from musculus C57BL/6J (male) was obtained from the Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/).
                                                                                                                                            /db_xref="taxon:10090"
/clone="UUGC2M0116E10"
                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL/6J"
                                                                 /hob_host="E. Coli strain XL10-Gold, T1-resistant, F
/hote="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                         /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                        /sex="Male"
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130773 MARC 1PIG Su
BE031984
BE031984.1 GI:8326
                                     Single pass sequencing. Bases ov 0.980904.e. Vector identified and -minmatch 12 options.
                                                                                                 USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, US
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                               1 (bases 1 to 586)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A.,
Stone, R.T., Heaton, M.P., Grosse, W.M., Benne
and Keele, J.W.
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FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                           Contact: Smith TPL
                                                                                                                                                                                                                                    Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota;
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Similarity 75.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
132 c 208 g 117 t
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Seq pr
                             Mus musculus
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BF578820
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602094862F1 NCI_CGAP_Co24
  Eukaryota;
Mammalia; F
                                                                    BF578820.1
                                             house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC lPIG"
/tissue_type="pooled"
/lab_host="DHIOB"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: Xhc Library made from pooled tissue from day 11, 13, 15, and 30 embryos."
3 a 169 c 163 g 141 +
  ; Metazoa;
Eutheria;
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ATTTAGGTGACACTATAG.
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55.3%;
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Rodentia;
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Pred. No. 2.5e-24;
0; Mismatches 249;
                                                                                                             Mus
Craniata; Ver
Sciurognathi;
                                                                                                             musculus
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              Vertebrata;
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  Muridae;
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ctcaatgctcgctacatgcacaagattcgcttccccatccctacagagatgattgtggtg
                                                                                                                             acaggcccagggtccatcgtctttaccttcattgacatttgcaaaaaacctcccccacacc
                                                                                                                                                                                               ggcctgcagatcctgatttcggtgctcaagtacatcttcggactgaccatcccctcctac
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                                                                                                                                                                                                                                                                  tttggctttgtggccatctacctctccgagtccttcatccggggcttcatgacggccgcc 633
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                                    AACATCGCAGACCTTGTGACATCTGTGATTATTCTAGTGGTCGTGTCGGTCTTTAAAGAA
                                                                   aacatcgcctcgctcatcttcgctctcatcagcggtgccttcctggtgctggtgaaggag
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                                                                                                                                                                                                                                                                                                                                                                                          AGAGTGGTCCTCA----
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plate: LLAM9774 row: l column:
High quality sequence stop: 658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 857)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
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/Glone=lib="NCI_CGAP_CO24"
/Glone_lib="NCI_CGAP_CO24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pcMV-SPORT6; Site_1
Site_2: Sall; Cloned unidirectionally. Primer:
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 223 c 195 g 227 t
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/strain="FVB/N"
/db_xref="taxon:1000"
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Pred. No. 3e-19;
0; Mismatches 261;
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Best Local Similarity
Matches 224; Conserv
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                         tcaagaactccctcaagcaactcaccgacccctactacctgtggaggaagagcaagctgg 1384
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       ACTCTGTCCTGGGGCAGGTGCCAGACACGGATATTTACAGAGATGTGGCAGAGTACTCAG
                                                                                              tggcagtgggtgtcgccttctccgtcctggtcgtggtcttcccagactcagttttcgaaatg 1504
                                                                                                                                                     ATCTGCTTATCTGGCTGGTGACCTTCACGGCCACCATCTTGCTGAACCTGGACCTTGGCT 180
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10614 row: g column: 09
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National Institutes of Health, Mammallan Gene
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BG680597 611 bp mrNA EST U1-MAY-ZUU1 602629036F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4753952 5',
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BG680597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
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/lab_host="DH10B (TI phage=resistant)"
/note="Organ: skin; Vector: pcWV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1:5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
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300-181-f03&t3=2000-03-31&t4=1)
Seq primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                   /note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                                                                                                tissue mRNA and cDNA amplification were performed low stringency conditions."
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/dev_stage="Adult"
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BB605137 RIKEN full-length enriched, 0 day neonate lung Mus
musculus cDNA clone E030008K16 5', mRNA sequence.
BB605137
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URL:http://genome.gsc.riken.go.jp/
Carninci.p., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
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Hanagaki,T., Hayatsu,N., Hiraoka,T., Hirozane,T., Hodoyama,Y.,
Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kawai,J., Kojima,Y., Konno
,H., Kusakabe,M., Matsuyama,T., Miyazaki,A., Nakamura,M., Nishi,K.,
Nomura,K., Numazaki,R., Okazaki,Y., Okido,T., Owa,C., Sakai,C.,
Sakai,K., Sasaki,D., Sato,K., Shibata,K., Shibata,Y., Shinagawa,A.,
Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Tanaka
,T., Toya,T., Watchiki,A., Yamamura,T., Yasunishi,A., Yoshida,K.,
Yoshiki,A., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci,P. and Hayashizaki,Y.
                                                                                                                                                                                                                                                               trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan: 81-45-503-9222
Fax: 81-45-503-9216
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Contact: Yoshihide Hayashizaki
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                                                                          visit our web site (http://genome.rtc.riken.go.jp) for
                         Location/Qualifiers
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346420 MARC 1PIG Sus s
BG732794 BG732794.1 GI:1401907
EST
                             USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, US
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                           Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., and Keele,J.W.
                                                                                               Contact: Smith TPL
                                                                                                          Unpublished (2000)
                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                         Sus scrota
                Email: smith@email.marc.usda.gov
                                                                                                                                             Design and use of two pooled tissue normalized cDNA
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/dev_stage="0 day neonate"
/lab_host="DH10B"
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/clone_lib="RIKEN full-length enriched, 0 day neonate
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/db_xref="taxon:10090"
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Seq primer: ATTTAGGTGACACTATAG.
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 Eukaryota;
              Mus musculus
                          house mouse.
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/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
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Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
152 c 149 g 129 t
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                          tccgtcctggtcgtggtcttccagactcagtttcgaaatggctatgcactggcccaggtc 1524
                                                                                                                                                agcttcctctccttcttcctcagcctgccctatggtgtggcagtgggtgtcgccttc 1464
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TCCTTGCTGCTCGTGGTCCGAATGCAGCTGCCCCATTACTCCGTCCTGGGGCAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the retina tissue cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC 9643,
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Bonaldo, M.F., Lenno
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TAG_LIB=NIH_BMAP_Ret4_S2
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a 124 c 120 g 134 t
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/note="vector: pT713D-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_Ret4_S2 library is a subtracted library,
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CDNA Library Preparation: Leonard Ira Zon DNA Sequencing by:
CDNA Library Preparation: Leonard Ira Zon DNA Sequencing by:
Washington University Genome Sequencing Center Clone distribution:
Genome Systems, St. Louis, Missouri (web address:
Www.genomesystems.com) (email contact: info@genomesystems.com) and
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Fax: 314 286 1810
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                                                                                                                                                                      Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 468. Location/Qualifiers
                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
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AA871419
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IMAGE:1096207 5' similar to
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Mammalia; Eutheria;
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/db_xref="taxon:10090"
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/clone_lib="Barstead bowel
                                                                                      /organism="Mus musculus"
/strain="FVB/N"
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Rodentia;
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ORIGIN
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Best Local Similarity 58.7%;
Matches 209; Conservative
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                                                                        1525 atggacactgacatttatgtgaatcccaagacctataatagggcccaggatatccagggg 1584
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                                                         265 CCAGATACGGGTATTTATAGAGACGTGGCAGAATACTCTGGGGCCAAGGAGGTCCCGGGT 324
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Pred. No. 4e-16;
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Search completed: April 25, 2002, 13:42:26 Job time: 7981 sec

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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Comp
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US-09-265-691-4
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5208.349 Million cell updates/sec
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Sequence 513, App
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Sequence 477, App
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1.6	1.6	1.6	1.6	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7
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US-09-105-537-1	US-08-899-514-1	US-09-074-912-3 US-08-822-586-46	US-08-766-738-2	US-08-439-009A-3	US-07-642-734C-3	US-08-487-826B-15	US-09-082-092-9	US-08-923-137-2	US-09-385-028-1	US-09-385-028-13	US-09-385-028-15	US-09-142-648B-6	US-08-614-377A-6	US-08-194-290-6	US-09-318-448-13
Sequence 1, Appli	Sequence 1, Appli	Sequence 3, Appli Sequence 46, Appl	Sequence 2, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 15, Appl	Sequence 9, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 13, Appl	Sequence 15, Appl	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 13, Appl

ALIGNMENTS

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NAME/KEY:
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LOCATION:
US-08-424-567-1
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                                                                                                                                       TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENUTH: 2882 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/026,045
APILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
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                                                               FEATURE:
                                                                                MOLECULE TYPE:
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TOPOLOGY: lir
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APPLICANT:
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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                                          COUNTRY:
                                                     CITY: Washington,
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STREET: 30
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                                                     E: Foley & Lardner
3000 K Street, N.W.,
ashington, D.C.
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ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29, COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: TELECOMMUNICATION PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/711,928 FILING DATE: 11-SEP-1996 CLASSIFICATION: 435 REFERENCE/DOCKET NUMBER: 40 ELECOMMUNICATION INFORMATION: APPLICATION NUMBER: FILING DATE: 05-MAF CLASSIFICATION: APPLICATION NUMBER: US 0: FILING DATE: 17-APR-1995 CLASSIFICATION: 05-MAR-1993 SD 29,768 08/026,045 40399/354/NIHD .0 Version

(202)672-5300

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Best Local Similarity 51.7%;
Matches 798; Conservative
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TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2882 base pairs
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STRANDEDNESS: double
TOPOLOGY: linear
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US-09-184-937-1
; Sequence 1, Application US/09184937
; Patent No. 621087
; GENERAL INFORMATION:
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APPLICANT: PAPAS, Takis S.
TITLE OF INVENTION: COlon
TITLE OF INVENTION: Expre:
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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US-09-184-937-1
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2882 base pairs
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NAME: BENT, Stephen A.
REGISTRATION UNMBER: 29,768
REFERENCE/DOCKET NUMBER: 4039
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPHONE: (202)672-5399
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APPLICATION NUMBER: US,
FILING DATE:
CLASSIFICATION:
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TOPOLOGY: 11
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RESULT 4 US-09-385-982-129 Sequence 129, Application Patent No. 6262334

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                        ctctactttgccaactcagagatcttcaggcaaaaggtcatcg
                                                     AAAGATTATTATGATATGTATGAGCCAGAAGGAGTGAAAATTTTCAGATGTCCATCTCCT
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EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/098,639
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 129
LENGTH: 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: misc_feature
; LCCATION: (1)...(588)
; OTHER INFORMATION: n = A,T,C
US-09-385-982-129
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                                                                                               Sequence 513, Application US/09385982 Patent No. 6262334 GENERAL INFORMATION:
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APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND
TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCDNA-260XX
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Best Local Similarity
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APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENE
TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCONA-260XX
CURRENT APPLICATION NUMBER: US/09/38
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EARLIER APPLICATION NUMBER: 09/328,111
EARLIER FILING DATE: 1999-06-08
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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Pred. No. 9.7e-21;
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; TYPE: DNA
; ORGANISH: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(623)
; OTHER INFORMATION: n = A
US-09-385-982-513
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Matches 258; Conserva
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EARLIER APPLICATION NUMBER: 09/328,111
EARLIER FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/098,639
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Pred. No. 1.3e-18;
0; Mismatches 229;
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GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND
TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCDNA-260XX
CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 09/328,111

GENE

EXPRESSION

US-09-385-982-146

; Sequence 146, Application US/09385982 ; Patent No. 6262334

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RESULT 7
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; LOCATION: (1)...(475)
; OTHER INFORMATION: n = A,T,C
US-09-385-982-146
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EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/098,639
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
SOFTMARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 146
                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCDNA-260XX
                                                                                                                                                                                                                                                                 Sequence 477, Application US/09385982 Patent No. 6262334
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Best Local
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                                                                                         CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 09/328,111
EARLIER FILING DATE: 1999-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo s
FEATURE:
             EARLIER APPLICATION NUMBER: 60/098,639 EARLIER FILING DATE: 1998-08-31
                                                   EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
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Similarity 56.5%;
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Pred. No. 2.4e-17;
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; NAME/KEY: misc_feature
; LOCATION: (1)...(595)
; OTHER INFORMATION: n = A,T,C
US-09-385-982-477
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                                                                                                                                             APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GE
TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCDNA-260XX
CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 09/328,111
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
                                                                                                                                                                                                                                                                                                                                         US-09-385-982-491/c

: Sequence 491, Application US/09385982

: Patent No. 6262334
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Best Local S
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                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                              SEQ ID NO 491
LENGTH: 583
                                                                                             EARLIER APPLICATION NUMBER: 60/098,639
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
                                                                                 SOFTWARE: FastSEQ
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ORGANISM: Homo
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              ORGANISM:
                               TYPE: DNA
FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: (1)...(583)
; OTHER INFORMATION: n = A,T,C
.US-09-385-982-491
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Best Local Similarity
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                                                                      REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 3047
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)83-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
  INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1596 cacgtactgctcccctctctactttgccaactcagagatctttcaggcaaaaggtcatcg 1654
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                                                                                                                                                                                            FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SCHEIFLINGER, F. APPLICANT: FALKNER, F. G. TITLE OF INVENTION: RECOMBINUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1416 ctccttcttcctcagcctgccctatggtgtggcagtgggtgtcgccttctccgtcctggt 1475
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                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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1800 Diagonal Road,
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53.5%;
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RESULT 10
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US-08-232-463-14
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1171
                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                     APPLICANT: Koyama, Yasuji
APPLICANT: Horiuchi, Tatsuo
APPLICANT: Nakano, Elichi
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APPLICATION NUMBER: JP 01-338267 FILING DATE: 28-DEC-1989
                                           CLASSIFICATION:
                                                       APPLICATION NUMBER: UFILING DATE: 19901227
                                                                                                                                                                             ZIP:
                                                                                                                                                                                        COUNTRY:
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2.7%; Pred. No. 0.00
ative 214; Mismatches
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                                                                                                                                                                                                                                                                                            Productin of N-Acetylmannosamine Dehydrogenase
                                                                                                                                                                                                                                   Birch, McKie & Beckett
Circle, NW
                                                                     US/07/637,865
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No. 0.00063;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: 1
TITLE OF INVENTION: 5
TITLE OF INVENTION: 6
NUMBER OF SEQUENCES:
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APPLICANT:
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                          SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ORIGINAL SOURCE:
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LENGTH: 816 base pairs
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                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION: 1..813
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Bohenzky, Roy A.
Russo, James J.
                                                        PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                     U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Edelman, Isidore S. Moore, Patrick S.
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US/08/728,323A
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Best Local Similarity
Matches 158; Conserv
                                                                                                                                                                                                                                                                                     Sequence 20, Application US/08770379 Patent No. 5849564
                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                         APPLICANT:
APPLICANT:
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APPLICANT:
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REFERENCE/DOCKET NUMBER: 05;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEPAX: 212-391-0525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                            ADDRESSEE: Cooper & Dunham LLP
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NAME: White, John P.
REGISTRATION NUMBER: 28,
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                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                                                              NUMBER OF SEQUENCES:
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LOCATION:
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ZIP: 10036
                                                                   STATE:
                                                                                  CITY: New York
                                                                                               STREET:
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CLASSIFICATION:
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                                                                New York
                                                                                                1185 Avenue of the Americas
                                                  U.S.A.
                                                                                                                                                                                         Edelman, Isidore
Moore, Patrick S.
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                                                                                                                                                           POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
                                                                                                                                                                                                         Isidore S.
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                                                                                                                                                                                                                                                                           Sequence 20, Application Patent No. 6183751
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                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: Chang, Yuan
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INFORMATION FOR SEQ ID NO: 22
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                 TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS TITLE OF INVENTION: SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 52 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                    APPLICANT: Edelman, Isidore S. APPLICANT: Moore, Patrick S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                               CORRESPONDENCE ADDRESS:
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SOFTWARE: Patentl
                                         ADDRESSEE: Cooper & Dur
STREET: 1185 Avenue of
CITY: New York
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              COUNTRY:
                                STATE: New York
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10036
              U.S.A
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SYSTEM: PC-DOS/MS-DOS
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                                                                                 Cooper & Dunham LLP
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Pred. No. 0.027;
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                                                                                                        GENERAL INFORMATION:
APPLICANT: Horlick, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/1D903US1
                                                                                                                                                                                                                                           Sequence 2
Patent No.
                     SEQ ID NO 2
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                                  CURRENT APPLICATION NUMBER: US/CURRENT FILLING DATE: 1998-08-08 NUMBER OF SEQ ID NOS: 36 SOFTWARE: FastSEQ for Windows Vo
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LENGTH: 1931
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TOPOLOGY: lin
MOLECULE TYPE:
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5. 5976807
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(212) 391-0505
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US-09-130-114-2
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Patent No.
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Best Local Similarity 46.4%;
Matches 153; Conservative
                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 24-DEC-1997
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ZIP: 27709
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5. 6239264
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r: 3054 Cornwallis Road

Research Triangle Park

No. 6239264th Carolina
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Knechtle, Philipp
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Steiner, Sabine
Mohr, Christine
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Pred. No. 0.021;
0; Mismatches 177;
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US-08-998-416-211
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INFORMATION FOR SEQ ID NO: 21
SEQUENCE CHARACTERISTICS:
LENGTH: 735 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                              Matches 119;
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Best Local Similarity
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ORIGINAL SOURCE:
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                                                      GTGGTGGGCCAGAGCTGCGATGCATGGGCGCACAAGTCGCTTGAACCGTTGATGACCGTT
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Pred. No. 0.036;
0; Mismatches 123;
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Gaps

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Search completed: April 25, Job time: 9530 sec 2002, 14:39:50

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Listing first 45 summaries
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1 atgagccagcccaggccccg.....agaccctgaccgccctgtga 2262
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/SIDS1/gcgdata/geneseq/geneseqn/Na1981.DAT:*
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Copyright (c) 1993 - 2000 Comp
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Probe #1762 used t
Probe #1686 used t
Probe #14911 used
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Human; membrane trantithyroid; immurantithyroid; membrane trantidiarrheic; new antihelminthic; prevent wenkes disease; disease inflammatory disease inflammatory disease; Hacell proliferative Homo sapiens. Key CDS Key		Ø	ithyroid; ithyroid; idiarrhei ihelminth gnosis; pkes disea heimer's lammatory ves disea	Human membrane	29-AUG-2000	AAD00611;	T 1 611 AAD00611 sta		49.8	50.6	50.8	52	52.4	53.8	51 C	58.8	62.6 61.8	64	67.4	5 6 8	71.4	73.8	75. 4 73.8	75.4	85. 8	94.8	106.2	111.4	122	122.6
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	Location/ 322308 /*tag= a /product=		cane transport pro immunosuppressiv (c; neuroprotectiv ilc; protozozotet; racin se; diabetes; Par disease; depressi / disorder; AIDS; se; Hashimoto's trative disorder;	transport	t entry)		CDNA;		445 1287	2364	696 168	2311	2745	345	559	2449	573 2241	2006	583	165	446	2403	482 601	482	1981	2279	475 505	623	1227	1466
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	protein, MTRP-12 cDNA.			9 вр.	ALIGNMENTS	AAH98262 AAC76396	AAZ29468	AAF:65718 AAO11817	AAZ50490	AAZ 2946/ AAD 09568	AAH98677	AAF93622	AAZ50489	AAF93562 AAZ29466	AAC42229	AAA16486	AAI25272 AAI51390	AAI38525	AAH16739	AAI33476 AAH08573	AAI12132	AAZ50482	AAZ50481	AAA16141	AAA16508	080	902			
	:in-12"		RP-12; antiinflammatory; cytostatic; nimetic; antidiabetic; nootropic; peressant; nephrotropic; virucide; terial; neuroleptic; antigout; orane transport disorder; epilepsy; disease; neurological disorder; allergy; cophrenia; immune disorder; allergy; s disease; atherosclerosis; gout; is; microbial infection; cancer;						Drosophila EST-der Human ORFX ORF1951	Genomic P. chrysog	Novel human polynu N-acetylmannosamin	٠,٠	P. chrysogenum sut Human transporter	Human EST-derived	wheat sulphate per	ybean sulpha	cDNA encoding SRT P. chrysogenum sut	Arabidopsis thalia	colon	Probe #15205 for g	#7211	CDNA	#216	#206	sulph	Corn sulphate perm	colon	Human colon cancer	polynucleot	Human polynucleoti

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Best Local S
Matches 820
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24-NOV-1998;
22-DEC-1998;
26-FEB-1999;
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antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
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Novel plasma membrane associated proteins useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancer, immune response and neuronal disorde
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in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
and ovarian cancer and other cancers of the adrenal gland, bone, bone
marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
(b) immune disorders e.g. Addison's disease, altergies, autoimmune
haproiditis, diabetes mellitus, Crohn's
disease, multiple sclerosis, rheumatoid arthritis and ulcerative
colitis; (c) cardiovascular disorders such as myocardial ischaemias;
(d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
cepllepsy, and (f) infectious diseases such as viral, bacterial, fungal
and parasitic infections.
Note: The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AAM42347-AAM42415) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                    Human secreted
                                                                                            06-OCT-2000
                                                                                                                    AAC03684;
                                                                                                                                           AAC03684
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                                therapy;
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                                 chromosome mapping;
                                           expressed sequence
                                                                    protein 5'
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Pred. No. 8.5e-79
1; Mismatches
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                                 tag; secreted ss.
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Best Local Similarity
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   AAQ71399;
                                                             AAQ71399 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
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Pred. No. 1.6e-74;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                    DRA probes may be synthesized according to the DRA DNA sequence used to screen colon tissue samples for DRA mRNA. Absence of DR mRNA, and consequently DRA tumor suppressor protein, indicates tissue abnormality. The cDNA may have therapeutic activity.
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2882 BP; 839 A; 579 C; 595 G; 868 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Page 21-25; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated polypeptide that is down regulated in colon adenocarcinomas and adenomas - is used as an indicator of tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1994-303023/37.
P-PSDB; AAR60568.
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                                                                                                                                                                                                                                                                                                                                               Local Similarity
agctatgtggacacagcagccatggaggctgagaggctgcacgtgtcagctacgctagcc
                                        tctgtctgcagctggccccagagtcgaaattccaggtcttcaacaatgcc-accaatgag
                                                                                                                                        aatggcctctactccttcttccccctcctgacctacttcttcctggggggtgttcac
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n adenocarcinoma; diagnostic; therapeutic; ds.
                          gcagtttcaaaagcagtcccagatcgcaatgcaactactttgggattgcctaacaactcg
                                                                          cacatatccgtgggtccgtttccgattctgagtatgatggtgggactagcagtttcagga
                                                                                        cagatggtgccaggtacctttgccgttatcagcatcctggtggg------
                                                                                                                           {\tt tatgggttgtatgcatcctttttcccagccataatctaccttttcttcggcacttccaga}
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Pred. No. 2.4e-71
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                       sulfate transporter gene. The invention also describes; (A) a method for screening a human bone/cartilage disease treating agent including the steps: (1) transforming an animal cell with the above vector, (2) culturing the animal cell in the presence of a sample and (3) detecting the increase in the sulfate ion intake to the cell; (B) a drug preparation for the treatment of human bone/cartilage disease containing the above vector as the active component. The sulfate transporter gene-containing vector is high in expression efficiency. This sequence encodes the rat DTDST protein used in the method of the invention.
                                                                                                                                              transporter expression containing a DNA sequence encoding a mammalian sulfate transporter (expression product of the DTDST gene) and containing no DNA sequence of 5' translation region of the mammalian
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treatment; cell sulphate ion intake;
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Qy 밁 B Qγ Query Match Best Local Matches 166 644 cal Similarity 49.775; Conservative aaacttcgcaatgccttcagatgttcctcagccaagatcaaagctgtggtgttttgggctg.165 ctgcctgtgctctcctggctccccaagtacaagattaaagactacatcattcctgacctg 225 aagcttcagaagagttgccagtgtaatgcaaccaaaatcagaaataggatttttgatttt 10.7%; 49.3%; 0; Score 242.2; Pred. No. 2e Mismatches 2e-50 DB 758; 20; Indels Length 2792 38; Gaps 703 643 4

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The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a

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                 The present invention relates to single exon nucleic acid probes (SEI The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are use for antenatal diagnosis of human genetic disorders.
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Query Match Best Local Similarity

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Query Match Best Local : Matches

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8.7**%**; 48.1**%**;

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27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                      The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases
                                                                           Note: The sequence data for this patent did not form specification, but was obtained in electronic format
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                   The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.
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                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human cervical epithelial cells
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30-JUN-2000;
30-AUG-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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            Probe; human; breast disease; breast cancer; inflammatory disease; proliferative breast di
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Query Match
Best Local Similarity
Matches 548; Conserv
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26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
                                                                                                                                                                                           The present invention relates to novel single exon nucleic acid pro The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the hybridises at high stringency to a nucleic acid expressed in the human straing, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast fibrocystic changes, proliferative breast disease an non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the present in the property of the proper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
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27-SEP-2000;
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Best Local
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14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
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Note: The sequence data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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aggtcatggacactgacatttatgtgaatcccaagacctataatagggcccaggatatcc
                                             ccttctccgtcctggtcgtggtcttccagactcagtttcgaaatggctatgcactggccc
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DB; AAM39866.
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                                 tcttctccctgctgctcgtggtggtccggacacagatgccccactactctgtcctggggc
                                                                              tggtgaccttcacggccaccatcttgctgaacctggaccttggcttggtggttgcggtca
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Wang ;
Zhou
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2000US-0552317.
2000US-05598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0663036.
2000US-0727344.
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Wehrman T,
Goodrich
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58.7%;
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Xu C,
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Pred. No. 9.4
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e AJ,
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Zhang
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                   immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; heemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                            Novel nucleic acids and polypeptides, used as central nervous system injuries
                                                                                                                                                                                                                                                                                 WPI; 2001-442253/47.
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14-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chemokinetic;
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29-NOV-2000;
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                                                                                                                                                          invention relates to human nucleic acids (AAI57798-AAI61369) and encoded polypeptides (AAM38642-AAM42213) with nootropic,
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           for receptor activity, arthritis and inflammation, leukaemias
                                                                                                                                                                                                                                                                      AAM41652.
                                                                                                                                                                                                                                                                                                          Liu C,
Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                 HYSEQ INC
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2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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Wehrman T,
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Nu C, Xue AJ,
Drmanac RT;
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Yang Y,
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Zhang v
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Best Local Similarity
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Catino TJ,
Schlegel R;
                                    Novel nucleic acids useful for treating
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                                                                  WPI;
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27-JAN-1999;
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Dwivedi P,
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99US-0117393
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Ford DM,
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                                   proteins for identifying therapeutic agents diagnosing cancer, especially colon cancer
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Lewis ME, N
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Claim 16;

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SUMMARIES

SOURCE ORGANISI REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS	RESULT 1 AF337809 LOCUS DEFINITION ACCESSION VERSION KEYWORDS		3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Result No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 gaccggacatacccagtgggagagaacttcgcaatg---ccttcagatgttcctcagcc 138
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                                                                                                                     GAT----ACTTCTCCAGCATTGTCCTCA-----AGCTCGGCAGAAAATGATTCAATGATA 685
                                                                                                                                                ATANAGGAATGGCTTCTCAGTGACATCGTCTCTGGCATCAGCACTGGGCTGGTGGCTGTG
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                                                                   CCGTTTCCAGTTCTGAGCATGATGGTGGGAGTTGTAGTTACAAGAGTGGCCTCGGGCCTCC
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Submitted (17-JAN-2001) Section of Digestive Diseases, Yal
University School of Medicine, 333 Cedar Street-1080 LMP,
Haven, CT 06520-8019, USA
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AYGLYAAFFPVITYFFLGTSRHISVGPFPVLSMYGVVARDVYSTKAFGEEFKKTYGHHKTFLDHLKGCCS
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NDSHIEEKVMYAASVTVLGGITQLLGVLQIGFVVILSESLISGFTTAAAIHULVSQ
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SKLPVPIPIELIMTVLATGISYGCNEEQFFGVAVVGNNSLGFQPPITFSVEVFQDTIG
DCFGIAIVGFAVAFSVASVYSLKYDYPIDGNQELIALGVSNIFTGAFKGFAGSTALSR
SGVQESTGGKTQVAGLLSAVIYLIVIVAIGFLLQFLQKSVLAALAGHLKGHLKGHLKQFAE
IGRLMKKDKYDCLTHIMTFIFAIVLGLGLGLGLAASVAFQLLTIVFTCPFECTM
SKLPVETSTGKTQVAGLLSAVIYLIVIVAIGFLKQKLIDAVGFNPLRIILRKRNK
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NADLPLNITTIPKISLHSLILDFSAVSFLDISSMRGLRTILQEFIRIKVDVYIVGTDDD
FIDKLARCEFFDDEVTDSIFFLTIHDAILHIMMKKDYSTSKFNSSQEKERKFDFTINT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="down-regulated in adenoma protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Rattus norvegicus"
/db_xref="taxon:10116"
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Pred. No. 7.2e-73;
0; Mismatches 751; Indels 12; Gaps
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 TT 182	6 GAAGGAGTGAAAATTTTCAGATGTCCGTCTCCAATCTACTTCGCAAACATTGGTTTCT	76	DЬ
tc 1638	9 caggggattaaaatcatcacgtactgctcccctctctactttgccaactcagagatct	157	Ωy
CA 1765	9 caggtcatggacactgacatttatgtgaatcccaagacctataatagggcccaggata 	151 170	Ф
CT 170	6 GCATTTCAGCTCCTAACTATTGTGTTCAGGACCCAATTCCCAAAATGCAGCACACTGG	4	DЬ
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TG 16	6 ATCATGACCTTCATCTTTGCCATCGTCCTTGGGCTCGGATTAGGCCTGGCAGCAGCAGTG	G.	Db
rtc 145	9 gtagtgagcttcctctcctccttcttcctcagcctgccctatggtgtggcagtgggtg	139	Qy
66 15	6 ATGCAGTTTGCCGAGATAGGCAGGCTGTGGAAAAAGGATAAATACGATTGTTTAATCT	G i	. Dp
qq 13	9 aagcaactcaccgacccctactacctgtggaggaagagcgagc	ω.	Q :
tc 1338 1525	9 tatectotecetaagtotgtgetaggagecetgategetgtetagateteaagaaetece 	127	y Q
TG 146	6 GCGGGGCTTCTCGGCTGTCATTGTGCTGATAGTCATAGTTGCCATCGGATTTCTCC		В
tg 127	9 gccagcctgtgtgtgtctctggtggtgatgatcaccatgctggtcctggggatctatc	121	Qy
	6 GGGAGCACAGCCCTTTCCAGATCAGGGGTTCAGGAGAGCACGGGAGGCAAAACACAGG	134	Db
jtg 121	9 atttgctgtgcgctttctgtcactctggctgtggatggagctggaggaaaatcccagg	115	Qγ
CA 1		128	뫄
rc 115	9 caggagatgatcgctctcggctgcagcaacttctttggctccttctttaaaattcat	109	γo
 AAC 128	6 GTGGCCTTTTCAGTTGCTAGCGTGTATTCCCCTCAAATACGATTATCCCATTGATGG	_	문
10	9 atcaacctggctatgggccggaccctggccaacaagcacggctacgacgtggattcg		Qy
C	6 GTGGAAGTTTTCCAAGACACCATAGGAGACTGCTTTGGCATTGCCATTGTCGGCTTTTG	116	DЬ
)tc 103	9 gtotoacagiggaaggacatgataggoacagoottotocotagooatogigagotaog	97	γQ
AGT 116	6 TTTGGCGTGGCCGTGGTTGGGAACATGAGTCTTGGGTTTCAACCCCCTATTACCCCC	110	рь
rtg 978	9 tatcacatgcagatcgtgggagaaatccaacgcgggttccccaccccggtgtcgcctg	91	γQ
G	6 GAACTCATGACTGTAATTGCAACAGGCATATCCTATGGCTGTAACTTTGAACAGA	104	DЬ
1ag 918	9 gagatgattgtggtggtggtggcaacagctatctccggggggctgtaagatgcccaaaa	85	γQ
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ıca 858	9 gtgctggtgaaggagctcaatgctcgctacatgcacaagattcgcttccccatccct	79	Qy
TG 985	6 CAAATTCAGAAGACGAACATCGCAGACCTGGTGACATCTGTGATTATCCTCGTGGTCG	92	Дb
- (+	9 aacctccccacaccaacatcgcctcgctcatcttcgctctcatcagcggtgccttcc	73	Qy
TCA 925	6 ACGGTCCCAGCACACAGCGCACTTCTCTATATTCAAAGTCCTGGAGTCAGTC	86	ДD
ıaa 738	9 accatcccctcctacacaggcccagggtccatcgtctttaccttcattgacatttgca	67	Qy
TG 86		80	Db .
C	9 ttcatgacggccgccggcctgcagatcctgatttcggtgctcaagtacatcttcggac	61	γQ
GC 805		74	Dβ

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TITLE
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                               tccatccaggtcccacaaggcatggcatttgctctgctggccaaccttcctgcagtcaat
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                                                                              CCCCGGTATCCTGTGCGTGACTGGCTCCTGGGTGACCTGTTATCCGGCCTGAGTGTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (19-JUL-2000) Zentrum fuer Molekulare Neurobiologie, University of Hamburg, Falkenried 94, Hamburg 20251, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 2589)
Waldegger, S., Jentsc
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cloning and Characterization of Solute Carrier 26 Gene Family Genomics 72 (1), 43-50 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2889)
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complete cds
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MQLPQGLAYALLAGLPPYGLYSSFYPWFIYELGTSRHISVCTFAYWSVMVCSVTES
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VNLKGMLRQLSDMRSLMKANRADLLIWLVTFTATILLNLDLGLVVAVIFSLEDMRSNL
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VNLKGMVQVSSGDKMEDATANGQEDSKAPDGSTLKALGLPQDFDFHSLILDLGALSFVD
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1. .2589
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/codon_start=1
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Direct Submission
Submitted (16-JUN-2000) Finnish Genome Center, University
Helsinki, Tukholmankatu 2, Helsinki 00014, Finland
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YSSFYPVFIYELFGTSRHISVGTFAVMSVWVGSVTESLAPQALNDSMINETARDAARV
YSSFYLVLVGLFQVGLGLIRFGFVNTYLSEPLLVRGTTTAAAVOPVSOLKYVFGLHL
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ELITLLGATGISYGMGLKHRFEVDVYGNIPAGLVPPVAPMTQLFSKLVGSAFTIAVG
ELLTLLGATGISYGMGLKHRFEVDVYGNIPAGLVPPVAPMTQLFSKLVGSAFTIAVG
FAIAISLGKIFALHGYRVDSNQELVALGSNLIGGIFQCFPVSCSMSRGLVQESTGG
NGQVAGAISSLFILLIIVKLGELFHDLPKAVLAAIIIVNLKGMLRQLSDMRSLWKANR
ADLLIWIVTFTATILLMIDLGLVVAFYSPLALKOVGVDPFYSVLGQVPDTDIYRDVA
EYSBAKEVRGVVVFRSAFTVFFANAFFYSDALKQRGVDDFLISOKKKLLKAGEQLK
LKQLQKEEKLRKQAASFKGASVSINVNTSLEDMRSNNVEDCKMMQVSSGDKMEDATAN
GQEDSKAPDGSTLKALGLPQDDFHSLLLDLGALSFVDFVCKSLKNIFHDFREIEVEV
                    YMAACHSPVVSQLEAGHFFDASITKKHLFASVHDAVTFALQHPRPVPDSPVSVTRL
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/protein_id="AAF81911.1"
/db_xref="GI:8926613"
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/db_xref="taxon:9606"
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Mammalia; Eutheria; Rodentia;
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/gene="Dra"
           /gene="Dra"
131. .2404
                                                                                                                             Location/Qualifiers
                                                                                           /strain="FVB/N"
                                                                                                      /organism="Mus musculus"
                                   /dev_stage="adult"
1. .2629
                                                          /tissue_type="colon"
                                                                     /sex="female"
                                                                               /db_xref="taxon:10090"
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NDSFIEEKWWAAASVTVLSGIIQLLLGVLQVGFVVIYLSESLISGFTTAAAIHVLVSQ
LKFMLQLFVPAYSDFESIFKVLESVFTQJQKTNLADLVTSVILLVVFVFKEINQRYR
SKLPVPIPIJATGVSYGCNFEDRFGVAVVGNMSLGFQPPITPSVEVFQDTIG
DSFGIAIVGFAVAFSVASVYSLKYDYPIDGNDELJALGVSNIFTGAFKGFAGSTALSR
SGVQESTGGKTQVAGELSAVIVLIVIVAIGFLLQPLQKSVLAALALGHKKGKMLMQFAE
IGRLWKKDKYDCLIWIMTFIFAIVLGLGLGLAASVAFQLLTIVFTQFPKCSTLANVG
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/protein_id="AAD42784.1"
/db_xref="G1:539730"
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/translation="MIEAIGNOYVVARPVYSTKTFGEEFKKTHRHHKTFLDHLKGCCS
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AYGLYAAFFPVITYFFLGTSKHISVGFPFVLSMMVGVVTRVVDPNASSELSSSSTE
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ALKKIRKLQKRGLIQMTPKGFICTSDGFKDSDEELDNNQIEELDQPINTTDLPFDIDM
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/codon_start=1
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1 (bases 1 to 4113)
2 heng, J., Shen, W., He, D.Z., Long, K.B., Madison, L.D.
Prestin is the motor protein of cochlear outer hair
Nature 405 (6783), 149-155 (2000)
20279283
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Submitted (20-APR-2001) Internal Medicine, Ya.
333 Cedar Street, P.O. Box 208029, New Haven,
Location/Qualifiers
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LITLIGATGISYGVKLNDRFKVDVVGNITTGLIPPVAPKTELFATLVGNAFAIAVVGF
AIAISLGKIFALRHGYRVDSNQELVALGLSNLIGGFFQCFPVSCSMSRSLVQESTGGN
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DLLIMLVTFVATIILLNLDIGLAVSIVFSLLLIVVVRMQLPHYSVLGQVPDTDIYRDVAE
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Direct Submission
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JOURNAL MEDLINE REFERENCE AUTHORS TITLE JOURNAL VERSION KEYWORDS DEFINITION ACCESSION RESULT AF167411 FEATURES REFERENCE SOURCE LOCUS AUTHORS TITLE ORGANISM AF167411 Mus musculus AF167411 AF167411.1 G Expression pattern of the mouse ortholog of the Pendred's gene (Pds) suggests a key role for pendrin in the inner express. Natl. Acad. Sci. U.S.A. 96 (17), 9727-9732 (1999) Submitted (09-JUL-1999) Direct Submission Everett, L.A. 99380587 National Institutes of MD 20892-4431, USA Everett, L.A., Morsli, H., Wu, D.K. and Green, E. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus musculus house mouse (bases 1 to 3086) erett, L.A. and Green, (bases 1 to 3086) Location/Qualifiers GI:5802226 3086 bp pendrin (Pds) E.D. Health, National Human Genome Research Institute, Health, 49 Convent Drive, MSC4431, Bethesd mRNA mRNA, complete ROD cds Muridae; Þ 29-AUG-1999 Euteleostomi; Murinae; Bethesda

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AAVVIANLKGMEMQVCDVPRLWKQNKTDAVIWVETCIMSIILGLDLGLLAGLLFALLT
VVLRYQEPSWNGLGSVPSTDIYKSITHYKNLEEPEGVKILRESSPIFYGNVDGFKKCI
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Tlrdslarscscsrkafgvvktlpildwlpkyrvkewllsbiisgvstglvgtlog
MayallaavpvQefll/saffepiltyfyvegtskhisvcepepvvslmygsvvlsmapdh
FLVPSGNGSALNSTTLDTGTRDAARVLLASTLTLLVGIIQLVFGGLQIGFIVRYLADP
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/strain="BALB/c"
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Direct Submission

Submitted (25-JAN-2001) NIDCD, NIH, Bl
Brive, Bethesda, MD 20892-4163, USA
On Jul 17, 2001 this sequence version

Location/Qualifiers
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Adler, H.J., Merritt, R.C.
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Adler,H.J., Merrittt,R.C. Jr., Belyantseva,I.A.
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TPEA"
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                                                                                                                                                                                                                                                                                                                                                  Score 337.2; DB 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jacob, P., Rossmann, H., Lamprecht, G., Kretz, A., Neff, C., Lin-Wu, Gregor, M. and Seidler, U.
Characterization of rat and rabbit brush border membrane anion
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Eukaryota; I
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Oryctolagus cuniculus
partial cds
AF314819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rossmann, H., Jacob, P. and Seidler, U. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exchange and Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
1 (bases 1 to 1389)
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                                                                        Conservative
                                                                                                                                                                                                      /product="down-regulated in adenoma DRA"
/protein_id="AK00897.1"
/db_xref="Gi:12656494"
/translation="FPIASWLPEYKLKEWLLSDIVSGISTGLVAVLQGLAFALLVNIP
PAYGLYAAFEPVLVYFFFGTSKHISVGPFPVLSMWGAAVVRLAPDDSISTDPSNNST
DBSCHNKRIMVAASVTFLTGGIQLAFGILRIGFVVIXLSEALISAFTTAAALHVVISQ
DBSCHNKRIMVAASVTFLTGGIQLAFGILRIGFVVIXLSEALISAFTTAAALHVVISQ
LKFMLQLTVPAHTOPFSIFKVLESLFTQIRKTNIADLVTGRVIIVVIVFVFKEINERF
KAKLPVPIPIELLVTVLAAGLSYGCNFQQRFNVSVIGKMEKGFQAPAAPDTQVFQDAI
                                                                                                                                                         GDCFTIAIVGFVVAFSVASVYSLKYDYRIDGSQELIAFGLGNIVTGSFKGFAGSTALS
RSAVQESTGGKTQVAGVLSSVIVLIVIVAIGFLLEPLQKSVLSALALGNLKGMLKQFA
EIGRLWKKKVDCLIWIMTFIFAIVLGLGLGLAASVAFELLTIVFRTQFFKCTTLANI
GRSNIYKNRKDYS"
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                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="intestinal mucosa"
                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryctolagus cuniculus"
/db_xref="taxon:9986"
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Fakler,B.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (08-JAN-2001) Universitaet Tuebingen,
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Proc. Natl. Acad. Sci. U.S.A. 98 (7), 4178-4183
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Rattus norvegicus mRNA
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VHVFTSMLKYLFGVKTKRYSGIFSVVYSTVAVLQNVKNLNVCSLCVGLMVFGLLLGK
EFNERFKEKLPAPIPLEFFAVVMGTGISAGFNLHESYSVDVVGTLPLGGLLPPANPDTS
LFHLVVVDAIAIAIVGFSVTISMAKTLAKKHGYQVDGNQELIALGICNSIGSLFQTFS
ISCSLSRSLVQBGTGGKTQLAGCLASLMILLVILATGFLFESLPQAVLSAIVINUKKG
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IMGARRKAMRKYAKEVGUNANIANATVKVDAEVDGENATKPEEDDDVKFPIVIKT
FPEELQRFLPQCBUHTWILDFTQVNFMDSVGVKTLAGIVKEYGGVGIYVYLAGCSAQ
VVNDLTSNRFFENPALKELLFHSIHDAVLGSQVREAMAEQETTVLPPQEDMEPNATPT
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Gregor, M. and Seidler, U.
Characterization of rat and
exchange and DRA expression
Unpublished
                                                                                                                                 Rossmann,H., Jacob,P. and Seidler,U.
Direct Submission
Submitted (16-OCT-2000) Abteilung Innere Medizin I,
Tueblingen, Otfried-Mueller-Str. 10, Tuebingen 72076,
Location/Qualifiers
                                                                                                                                                                                                                                                                                              Rattus.
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partial cds.
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Mammalia; Eutheria;
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                                                    /organism="Rattus norvegicus"
/strain="Wistar rat"
/db_xref="taxon:10116"
/tissue_type="intestinal muco:
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LTIVFRYQFPKCSTLANVGRSNIYKNKKNYADVYEPECVKIFRCPSPIYFANIGFFKQ
KLIDAVGENPLRILKKRNKALKKIRKLQKQGLIQVTPKFFICTSDGFKDSDEELDNNQ
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Direct Submission
Direct Submission
Submitted (21-OCT-1997) Genome Technology Branch,
Genome Research Institute, National Institutes of
Convent Drive, Bethesda, MD 20892, USA
                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 4930)

Everett,L.A., Glaser,B., Beck,J.C., Idol,J.R., Buchs,A., Heyman,M., Adawi,F., Hazani,E., Nassir,E., Baxevanis,A.D., Sheffield,V.S. and
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                                                                Green, E.D
                                                                                          Everett, L.A.,
                                                                                                                                   transporter gene
Nature Genet. 17
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Pendred syndrome is caused by
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                               tgcagtttggctttgtggccatctacctctccgagtccttcatccggggcttcatgacgg 628
                                                                         TCCTGATTGCCAGTGCCCTGACTCTGCTGGTTGGAATTATACAGTTGATATTTGGTGGCT
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MAYALLAAVPYGYGLVSAFFPILTY FIGTSRHISVGFPPVSLMVGSVYLSMAPDEH
FLVSSGKGTVLNTTMIDTAARDTARVLISALTLLVGIIQLIFGGLOIGFIVRYLADP
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FLPPELPPVSLFSEMLAASFSIAVVAYAIAVSVGKYVATKYDYTIDGNQEFIAFGISN
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AAVVIANLKGMEMQLCDIPRLMRQNKIDAVIMVFTCIVSIILGLDLGLLAGLIFGLLT
VVLRVQFPSMNGLGSIFSTDIYKSTKNYNIEEEPQGVKLIRFSSPIFYGNVDGFKKCI
KSTVGFDAIRKYNKRLKALRIQKINGALTAGIISAAVSTRAVUAFEEPBDIEBL
EELDIPTKEIEIQVDMNSELPVKVNVPKVPIHSLVLDCGAISFLDVGVRSLRVIVKE
FORIDVNYTAASLQDYVIEKLEQCEFFDNIKKDTFFLTVHDAILYLQNQVKSQEGQG
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/protein_id="AAC51873.1"
/db_xref="G1:2654005"
/translation="MAAPGGRSEPPQLPEYSCSYMVSRPVYSELAFQQQHERRLQERK
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/db_xref="taxon:9606"
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TATGGGTTGTATGCATCCTTTTTCCCAGCCATAATCTACCTTTTCTTCGGCACTTCCAGA
                                                                       ggatccatccaggtcccacaaggcatggcatttgctctgctggccaaccttcctgcagtc
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Schweinfest, C.W., Henderson, K.W.,
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IDFTINTNGGLRNRVYEVPVETKF"
1 578 c 596 g 868 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Nuclear localization signal at AA 569-573,
579-583; acidic transcr. activ. domain 620-640;;
motif 653-676"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAA58443.1"
/db_xref="GI:291964"
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185. .2479
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185. 2479
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/db_xref="taxon:9606"
/cell_type="epithelial cell"
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G18336.1
                                                                                                                                                                                                    Email: egreen@nhgri.nih.gov
Primer A: TCACCACATAGTTGCAAAGG
Primer B: GCATTTGTAGAATACACTGG
STS size: 113
PCR Profile:
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Green, E.D.
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                                                                                                                                                                                                                                                                                Contact: Eric D. Green
Genome Technology Branch
National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08,
                                                                                                                                                                                                                                                            Tel: 3014020201
Fax: 3014024735
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: sp_bacteria
3: sp_fungi:*
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  April 26, 2002, 09:04:29; Search time 32.14 Seconds (without alignments) 3426.978 Million cell updates/sec
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3869
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sp_unclassified:*
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            O9beg8 bos taurus
O99jy3 ovis aries
O99bgh1 oryctolagus
O99pd9 rattus norv
O9h2b4 homo sapien
O9vvm6 drosophila
O23454 caenorhabdi
O17951 caenorhabdi
O17951 caenorhabdi
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O17951 caenorhabdi
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Q9eph0 rattus norv
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Q9r155 mus musculu
Q9r154 rattus norv
Q9wvc8 mus musculu
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VGEKLRNAFRCSSAKIKAVVFGLLFVLSWLPKYKIKDYIIPDLLGGLSGGSIQVPQGMA 	Score 1258; DB 4; Length Pred. No. 9.8e-71; Pred. No. 9.8e-71; Indel:	99SEV7 99ATHF7 99ATHF7 99ATHF7 99ATHF7 99ATH12 33167 231250 99SY13 99SY13 99SY13 99SY147 99SY448 299SY448 299AT48 99AT48
SGGSIQVPQGMA 91 : : : SVAIMQLPQGLA 89	th 738; els 52; Gaps 8;	Q9sev7 guillardia 004001 sporobolus Q9fy46 arabidopsis Q9fy46 arabidopsis Q9fy46 arabidopsis Q9at12 zea mays (m Q23167 caenorhabdi Q49307 arabidopsis Q9sx52 arabidopsis Q9sx52 arabidopsis Q9sx52 arabidopsis Q5025 arabidopsis Q65025 arabidopsis Q65025 arabidopsis Q9x9b5 aegilops ta Q44016 caenorhabdi Q44348 bordeum vul Q9at47 lycopersico Q64435 arabidopsis Q9yab7 arabidopsis Q91w86 arabidopsis Q91w86 arabidopsis Q91w86 arabidopsis Q91w86 arabidopsis Q91w87 arabidopsis Q91w87 arabidopsis Q91w87 arabidopsis Q91w48 lycopersico Q9fpq7 arabidopsis Q9fpq7 arabidopsis Q9fpq4 solanum tub Q91m44 arabidopsis

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Best Local Sim
Matches 261;
                                                                                                                                      "Cloning and Characterization of Carrier 26 Gene Family.";
Genomics 72:43-50(2001).
EMBL; AF288410; AAKI9153.1; -
SEQUENCE 759 AA; 82966 MW;
                                                                                                                                                                                                                                                                                                                            Q9BXS9;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
SOLUTE CARRIER FAMILY 26 MEMBER 6.
                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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FALLANLPAVNGLYSSFFPLLTYFFLGGVHQMVPGTFAVISILVGNICLQLAPESKFQVF
                        PRTHQWRTWLQCSRARAYALLLQHLPVLVWLPRYPVRDWLLGDLLSGLSVAIMQLPQGLA
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                                                                         Score 1258; DB 4;
Pred. No. 1e-70;
2; Mismatches 238;
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"The reciprocal electromechanical properties of molecule of rat outer hair cells."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ da EMBL; AJ303372; CAC21555.1; ...
InterPro; IPR002645; STAS.
InterPro; IPR001902; Sulfate_transp.
Pfam; PF01740; STAS: 1.1
Pfam; PF00916; Sulfate_transp; 1.
SEQUENCE 744 AA; 81278 MW; E49E842CF7A3CD58
                                                                                                                                                             Eukaryota; Métazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                       Q9EPHO;
                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                       SEQUENCE FROM N.A.
Ludwig J., Oliver D., Frank G.,
                                                                                                                                                                                                     Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SSPAQSEPPASAEAPGEPSDMLASVPPFVTFHTLILDMSGVSFVDLMGIKALAKLSSTYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIYRDVAEYSEAKEVRGVKVFRSSATVYFANAEFYSDALKQRCGVDVDFLISQKKKLLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIYVNPKTYNRAQDIQGIKIITYCSPLYFANSEIF------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRSLVQESTGGNSQVAGAISSLFILLIIVKLGELFHDLPKAVLAAIIIVNLKGMLRQLSD
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                                                                                                                                                                                                                                                                                     PRELIMINARY;
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Last sequence update)
Last annotation update)
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E49E842CF7A3CD58 CRC64
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; Murinae; Rat
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Query Match Best Local S Matches 265

Similarity

32.5%; 163;

Score 1255.5; DB 11; Pred. No. 1.4e-70;

Mismatches

Indels

Gaps

11;

Length

744;

265;

Conservative

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Q9JKQ2;
Q1-OCT-2000
01-OCT-2000
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PRESTIN.
SEQUENCE FROM N.A.
MEDLINE=20279283; PubMed=10821263;
Zheng J., Shen W., He D.Z.Z., Long
"Prestin is the motor protein of co
                                                                                                                                Meriones unguiculatus (Mongolian jird).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
Meriones.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TFSPDSSSPAQSE-----PPASAEAPGEPSDMLASVPPFVTFHTLILDMSGVSFVDLMGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GSQVREAMAEQETTVLPPQEDM
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(TrEMBLrel. 15, Last sequence up
(TrEMBLrel. 17, Last annotation
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RESULT Q99NH7 ID QS AC QS DT 01 DT 01 DT 01

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Q99NH7; Q99NH7; 01-JUN-2001 01-JUN-2001 01-JUN-2001

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Best Local
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EMBL; AF230376; AAF71715.1; -.

InterPro; IPR002645; STAS.

InterPro; IPR001902; Sulfate_tra
Pfam; PF01740; STAS; 1.

Pfam; PF00916; Sulfate_transp; 1
SEQUENCE 744 AA; 81418 MW; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KYHVERDIFSHPVLQERLHVKDKVSESIGDKLKQAFTCTPKKIRNIIYMFLPITKWLPAY
                                                 LSSTYGKIGVKVFLVNIHAQVYNDISHGGVFEDGSLECKHVFPSIHDAVLFAQANARDVT
                                                                                         TFSPDSSSPAQSEPPASAEAPGEPSDMLASVPPFVTFHTLILDMSGVSFVDLMGIKALAK
                                                                                                                     YANSDLYSNALKRKTGVNPALIMGARRKAMRKYAKEVGNA--NIANAAVVKVDGEVDGEN
                                                                                                                                        FANSEIFRQKVIAKT-----VSLQELQQDFENAPPTDPNNNQTPANGTSVSYI
                                                                                                                                                                          YGVAVGVAFSVLVVVFQTQFRNGYALAQVMDTDIYVNPKTYNRAQDIQGIKIITYCSPLY
                                                                                                                                                                                                                                                                                GFNLHESYSVDVVGTLPLGLLPPANPDTSLFHLVYVDAIAIAIVGFSVTISMAKTLANKH
                                                                                                                                                                                                                                                                                         GCKMPKKYHMQIVGEIQRGFPTPVSPVVSQWKDMIGTAFSLAIVSYVINLAMGRTLANKH
                                                                                                                                                                                                                                                                                                                      LQNVKNLNVCSLGVGLMVFGLLLGG-----KEFNERFKEKLPAPIPLEFFAVVMGTGISA
                                                                                                                                                                                                                                                                                                                                  CKNLPHTNIASL----IFALISGAFLVLVKELNARYMHKIRFPIPTEMIVVVVATAISG
                                        MVKEYGDVGIYVYLAGCSPQVVNDLTRNRFFENPALK-ELLFHSIHDAVL----
                                                                              ATKPEEEDDEVKYPPIVIKTT-FPEELQRFMPQTENVHTIILDFTQVNFIDSVGVKTLAV
                                                                                                                                                           YGLTTAVIIALLTVIYRTQSPSYKVLGQLPDTDVYIDIDAYEEVKEIPGIKIFQINAPIY
                   PGHNFQGAPGDAELSLYDSEEDI
-GSHVREAMAEQEASAPPPQDDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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Sulfate_transp.
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Best Local Similarity 36.5
Conservative
Q9R155;
Q9R155;
Q1-MAY-2000
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=ORGAN OF CORTI;
STRAIN=C57BL/6; TISSUE=ORGAN OF CORTI;
Adler H.J., Merritt R.C. Jr., Belyantseva I.A.,
"Mus musculus organ of Corti mRNA for prestin.",
"Mus musculus organ of Corti mRNA for prestin.",
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ da
EMBL; AY024359; AAG59999.1; -
SEQUENCE 744 AA; 81380 MW; 56E842748288E96F
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
MCBI_TaxID-10090;
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   (TrEMBLrel. 13,
                                         PRELIMINARY;
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MEDLINE-99380587; PubMed-10449762;
Everett L.A., Morsli H., Wu D.K., Green E.D.;
"Expression Pattern of the Mouse Ortholog of the Pendi
(Pds) Suggests a Key Role for Pendrin in the Inner Ear
Proc. Natl. Acad. Sci. U.S.A. 96:9727-9732(1999).
EMBL; AP167411; AAD51617.1; .
EMBL; AP167411; AAD51617.1; .

MCD; MGI:1346029; S1C2644.
R InterPro; IPR001902; STAS.
InterPro; IPR001902; Sulfate_transp.
Pfam; PF001740; STAS; 1.
R Pfam; PF0016; Sulfate_transp: 1.
R Pfam; PF00916; Sulfate_transp: 1.
R Pfam; PF00916; Sulfate_transp: 1.
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01-JUN-2001 (TrEMBLrel.
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SLC26A4 OR PDS.
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Mammalia; Eutheria;
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TFSPDSSSPAQSEPPASAEAPGE----PSDMLASVP----PFVTFHTLILDMSGVSFVD
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Metazoa; Rodentia;
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L%; Pred. No. 3.8e-66;
147; Mismatches 297
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AFEPDE----DVEEPEELNIPTKEIEIQVDWNSELPVKVNVPKVPIHSLVLDCGAVSFLD

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RESULT
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Best Local Similarity
Matches 264; Conserv
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01-MAY-2000
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9R154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Expression Pattern of the Mouse Ortholog of the Pendred (Pds) Suggests a Key Role for Pendrin in the Inner Ear."; Proc. Natl. Acad. Sci. U.S.A. 96:9727-9732(1999).

EMBL; AF167412; AAD51618 1; -
InterPro; IPR001902; Sulfate_transp.
InterPro; IPR002645; STAS.
Pfam; PF00916; Sulfate_transp; 1.
Pfam; PF00916; Sulfate_transp; 1.
Pfam; PF01740; STAS; 1.
PROSITE; PS01130; SULFATE_TRANSP; UNKNOWN_1.
SEQUENCE 780 AA; 85714 MW; DAOCDB7496BBD535 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99380587; PubMed=10449762; Everett L.A., Morsli H., Wu D.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                          LPKYKIKDYIIPDLLGGLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLGGVH 12:
FTFIDICKNLPHTNIASLIFALISGAFLVLVKELNARYMHKIRFPIPTEMIVVVVATAIS
                                                                                                                                                                                                                  LVGIIQLVFGGLQIGFIVRYLADPLVGGFTTAAAFQVLVSQLKIVLNVSTKNYNGVLSII
                                                                                                                                                                                                                                                                           HISVGPFPVVSLMVGSVVLSMAPDDHFLVPSGNGSTLNTTTLDTGTRDAARVLLASTLTL
                                                                                                                                                                                                                                                                                                                                                                                          YAVSRPVYSELAFQ----QQRERRLPERRTLRDSLARSCSCSRKRA--FGALKALLPILDW 74
                                                                                                                                                                                                                                                                                                                                                                                                                     YVVDRAAYSLTLEDDEFEKKDRTYPVGEKLRN--AFRCSSAKIKAVVFG----LLPVLSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQNQVKS-------REGQDSLLETVARIRDCKDPLDLMEAEM-----NAEEL
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                                                                                                 YGANLEANYNAGIVKSIPSGFLPPVLPSVGLFSDMLAASFSIAVVAYAIAVSVGKVYATK
                                                                                                                           GGCKMPKKYHMQIVGEIQRGFPTPVSPVVSQWKDMIGTAFSLAIVSYVINLAMGRTLANK
                                                                                                                                                         YTLIEIFQNIGDTNIADFIAGLLTIIVCMAVKELNDRFKHKIPVPIPIEVIVTIIATAIS
                                                                                                                                                                                                                                             LTAIIQMGLGFMQFGFVAIYLSESFIRGFMTAAGLQILISVLKYIFGLTIPSYTGPGSIV 238
                                                                                                                                                                                                                                                                                                                                  LPKYRVKEWLLSDIISGVSTGLVGTLQGMAYALLAAVPVQYGLYSAFFPILTYFVFGTSR
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                                          HDYIIDGNQEFIAFGISNVFSGFFSCFVATTALSRTAVQESTGGKTQVAGLISAVIVMVA
                                                                   HGYDVDSNQEMIALGCSNFFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMIT
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0 (TrEMBLrel. 13, 1
1 (TrEMBLrel. 17,
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1184; DB 11
Pred. No. 4.4e-66;
13; Mismatches 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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Best Local
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DOWN-REGULATED IN ADENOMA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-FURNE TISSUE=COLON;
STRAIN-FURNE; TISSUE=COLON;
Melvin J.E., Park K., Richardson L.A., Schultheis P.J., Shull G.E.
"Mouse Down-Regulated in Adenoma (DRA) is an Intestinal C1-/HCO3-
"Mouse Down-Regulated in Colon of Mice Lacking the NHE3 Na-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002645; STAS.
InterPro; IPR001902; Sulfate_transp.
InterPro; IPR001902; Sulfate_transp.
Pfam; pF001740; STAS; 1.
PROSITE; PS01130; SULFATE_TRANSP; UNKNOWN_1.
SEQUENCE 757 AA; 83589 MW; 32B1AC648BE74A07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Exchanger.";
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                                                                                                                                                                                                                                                                                                                                                                        RYVVDRAAYSLTLFDDEFEKKDRTYPVG-EKLRNAFRCSSAKIKAVVFGLLPVLSWLPKY 65
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                                                                                                                                        GTFAVISILVGNICLQLA--PESKFQVFNNAT-NESYVDTAAMEAERLHVSATLACLTAI 182
                                                                                                                                                                                                                                                       KIKDYIIPDLLGGLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLGGVHQMVP 125
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                             GPFPVLSMMVGVVVTRVVSDPNASSELSSSSTENDSFIE-----
                                                                                                                                                                                                                          KIKEWLLSDIVSGISTGLVAVLQGLAFALLVNIPPAYGLYAAFFPVITYFFLGTSRHISV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFAQANAR
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IQLLLGVLQVGFVVIYLSESLISGFTTAAAIHVLVSQLKFMLQLPVPAYSDPFSIFKVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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Pred. No. 8.2e-
19; Mismatches
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                                                                                                              EKVMVAASVTVLSGI
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                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 231
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DTD SULFATE TRANSPORTER.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Baumgartner B.G., Kriegesmann B., Brenig B.;

"Cloning and characterization of the bovine DTD sulfate (bDTDST) gene.";

Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases EMBL; AJ232515; CAB69640.1;

SEQUENCE 734 AA; 81540 MW; D5224A27EA5D691E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9BEG8
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ILLVPQSIAYSLLAGQEPIYGLYTSFFASLIYFILGTSRHISVGIFGILCLMIGEVVDRE
                                                                                                                    EKSDNNFKKFVIKKLEKSCQCSSTKAKNTIFGFLPVLQWLPKYDLKKNILGDVMSGLIVG
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32.8%;
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Pred. No. 1.2e-
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Kriegesmann B., Baumgartner B.G., Deppe A., Brenig B.;
"Sequence of the ovine sulfate transporter gene.";
submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; Y18558; CAC20729.1; -.
InterPro; IPR002645; STAS.
InterPro; IPR001902; Sulfate_transp.
Pfam; pF01740; STAS; 1.
Pfam; PF01740; STAS; 1.
PROSITE; PS01130; SULFATE_TRANSP; 1.
SEQUENCE 734 AA; 81439 MW; 35EABDFB4F2F3B36 CRC64;
                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Caprinae; Ovis. NCBI_TaxID=9940;
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01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2001 (TrEMBLrel. 17,
SULFATE TRANSPORTER.
                                                                                                                                                                                                                                      Ovis aries (Sheep).
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                                                                                                                                                SEQUENCE FROM N.A.
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Query Match Best Local Similarity Matches 229; Conserv

Conservative

25.9%; 33.2%; 132;

Score 1001.5; DB Pred. No. 1.1e-54; 32; Mismatches 281

281; 6;

Indels Length

47;

Gaps

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RESULT 11
Q9BCH1
AC Q9BCH1
AC Q9BCH1
DT 01-JUN
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                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Ci
Mammalia; Eutheria; Lagomorpha;
                                                                                                                                                                                                                                                                                                                Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; C
                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrembLrel. 17, 01-JUN-2001 (TrembLrel. 17, 01-JUN-2001 (TrembLrel. 17, 01-JUN-REGULATED IN ADENOMA DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9BGH1
     NON_TER
                                               "Characterization of rat and rabbit brush border membrane exchange and DRA expression in rabbit, rat, and human duck submitted (CCT-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF314819; AAK00897.1; •.
                                                                                                                                       Jacob P., Rossmann H., Lamprecht Gregor M., Seidler U.;
                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-INTESTINAL MUCOSA;
                                                                                                                                                                                                                                                                  NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                    SLC26A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9BGH1;
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                                                                                                                                                                          EMBL; AF314820; AAKÓO898.1;

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NON_TER 545 545

SEQUENCE 545 AA; 59322 MV
                                                                                                                                                                                                                                                                                                            Gregor M., Seidler U.; "Characterization of rat and rabbit brush border membrane
                                                                                                                                                                                                                                                                                                                                 Jacob P., Rossmann H., Gregor M., Seidler U.;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-WISTAR RAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVLSWLPKYKIKDYIIPDLLGGLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFF 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVTFLTGIIQLAFGILRIGFVVIYLSEALISAFTTAAALHVVISQLKFMLQLTVPAHTDP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLACLTAIIQMGLGEMQEGEVAIYLSESFIRGEMTAAGLQILISVLKYIFGLTIPSYTGP 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLPAVNGLYSSFFPLLTYFFLGGVHQMVPGTFAVISILVGNICLQLAPESKFQVFNNATN 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IVLGLGLGLAASVAFELLTIVFRTQFPKCTTLANIGRSNIYKNRKDYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FFLSLPYGVAVGVAFSVLVVVFQTQFRNGYALAQVMDTDIYVNPKTYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVMITMLVLGIYLYPLPKSVLGALIAVNLKNSLKQLTDPYYLWRKSKLDCCIWVVSFLSS 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLANKHGYDVDSNQEMIALGCSNFFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSL 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATAISGGCKMPKKYHMQIVGEIQRGFPTPVSPVVSQWKDMIGTAFSLAIVSYVINLAMGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VYSLKYDYRIDGSQELIAFGLGNIVTGSFKGFAGSTALSRSAVQESTGGKTQVAGVLSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGLSYGCNFQQRENVSVIGKMEKGFQAPAAPDTQVFQDAIGDCFTIAIVGFVVAFSVAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IVLIVIVAIGFLLEPLQKSVLSALALGNLKGMLMQFAEIGRLWKKDKYDCLIWIMTFIFA
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182; Conser
                                                                 al Similarity
183; Conser
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nilarity 38.9%;
Conservative 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation updat
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADENOMA
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                                                                                      22.8%;
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                                                                 94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 914.5; |
Pred. No. 1.6e
)5; Mismatches
                                                            Score 882.5; DB 11;
Pred. No. 2e-47;
4; Mismatches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                      Query Match
Best Local Sim
Matches 209;
                                                                                                                           Exchanger.";

Genomics 70:102-112(2000).

Genomics 70:102-112(2000).

EMBL; AF297659; AAG22075.1; .

EMBL; AF297659; AAG22075.1; .

EnterPro; IPR003880; Phosphopant_attach.

InterPro; IPR001902; Sulfate_transp.

Pfam; PF01740; STAS; 1.

Pfam; PF00916; Sulfate_transp; 1.

PFAm; PF00916; Sulfate_transp; 1.

PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.

SEQUENCE 701 AA; 74991 MW; F37DC87F6A036676 CR
                                                                                                                                                                                                                                                                         Lohi H.,
Kere J.;
                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
SULFATE/ANION TRANSPORTER SAT-1 PROTEIN.
SLC26Al.
                                                                                                                                                                                                                                                 "Mapping of Five New Characterization of 9
                                                                                                                                                                                                                                                                               MEDLINE-20541715; PubMed-11087667;
Lohi H., Kujala M., Kerkela E., Saarialho-Kere U.,
                                                                                                                                                                                                                                                                                                          TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9H2B4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9H2B4
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     419
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                                    RTYPVGEKLRNAFR------CSSAKIKAVVFGLLPVLSWLPKYKIKDYIIPDLLGGLS
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| | : :|:|| ||:|||| |:||:|
| KKNYADVYEPEGVKIFRCPSPIYFANIGFFKQKLI 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKSKLDCCIWVVSFLSSFFLSLPYGVAVGVAFSVLVVVFQTQFRNGYALAQVMDTDIYVN
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                         RQRPAPRGLREMLKARLWCSCSCSVLCVRALVQDLLPATRWLRQYRPREYLAGDVMSGLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKDKYDCLIWIMTFIFAIVLGLGLGLAASVAFQLLTIVFRTQFPKCSTLANVGRSNIYKN
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                                                                                 Similarity
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Primates;
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                                                                               29.6%;
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                                                                      146;
                                                                               Score 878; DB 4;
Pred. No. 5.2e-47;
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Candidate Gene for
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                                                                     Mismatches
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Q9VVM6;
Q1-MAY-2000 (TrEMBLrel. 13, C
Q1-MAY-2000 (TrEMBLrel. 13, I
Q1-JUN-2001 (TrEMBLrel. 17, I
CG5485 PROTEIN.
CG5485.
MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ephydroidea; Drosophilidae;
NCBI_TaxID=7227;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01740; STAS; 1.
Pfam; PF00916; Sulfate_transp; SEQUENCE 742 AA; 80315 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunkov B.C., Dunkov B.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase; FBgn0036770; CG5485.
InterPro; IPR002645; STAS.
InterPro; IPR001902; Sulfate_transp
  442
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                                                                                                                                                                                                          LKNSLKQLTDPYYLWRKSKLDCCIWVVSFLSSFFLSLPYGVAVGVAFSVLVVVFQTQFRN
                                                                                                                            GAFLVLVKE-LNARYMHKIRFÐIÐTEMIVVVVATAISGGCKMÞKKYHMQIVGEIQRGFÐT
                                                                                                                                                              LVNGFTTAAACHVVTAQLKDVLGISVPRHKGAFKIIYTVIDVIKGVPQTNLVNFGFCMAV
                                                                                                                                                                                                                                                                                                               FKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMITMLVLGIYLYPLPKSVLGALIAVN 441
                                                                                PVSPVVSQWKDMIGTAFSLAIVSYVINLAMGRTLANKHGYDVDSNQEMIALGCSNFFGSF
                       FSCIPMACSLSRSVIQDQTGGVSQIASLVSASLVVVTLMWIGPFFSSLPRCVLAGVIIVA
                                                                   PVLPRLDLVPKVAVDSIAIAIVTYSIIMSMGLTFAKKHGYEVRPNQELFAMGIGNMVGGC
                                                                                                               IAFMMICNEILKPRLSKKCRFPLPAELIMVIGGTLISKWFNLYVDYNVNPVGKIPSGLPE
                                                                                                                                                                                  FIRGEMTAAGLQILISVLKYIFGLTIPSYTGPGSIVFTFIDICKNLPHTNIASLIFALIS 262
                                                                                                                                                                                                                                                      GTSKHISIGTFAVASMMTAKVVDTYANVDDHHQILPINAFGLQSNGTATASPLLLINSSA
                                                                                                                                                                                                                                                                             GGVHQMVPGTFAVISILVGNIC------LQLAPESKFQVFNNAT------NES
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                                                                                                                                                                                                                                                                                                    ILQWLPQYSPRRDLPGDIIAGFTVAIMNIPHGMAYGILAGVSAGNGLYMAVFPVLAYMFL
                                                                                                                                                                                                                                                                                                                                                                                              Conservative 158; Mismatches 301; Indels
                                                                                                                                                                                                                               ----AAMEAE----RLHVSATLACLTAIIQMGLGFMQFGFVAIYLSES
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28.3%;
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Pred. No. 2.4e-45;
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E68FC76976312207 CRC64:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                     Pfam; PF00916; Sulfate_transp; Pfam; PF01740; STAS; 1.
SEQUENCE 611 AA; 67595 MW;
                                                                                                                                                                                                                                                                                                                "2.2 Mb of contiguous nucleotide sequence from chromosome elegans.";
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01-NOV-1996 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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EMBL; 270757; CAA94798.
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InterPro; IPR002645; STAS.
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GLTVGIMHVPQGMAYASLAGVPPVYGMXSSFFASTIYMFFGTARHISIGVFAVASMMVGA
                 GLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLGGVHQMVPGTFAVISILVGN 137
                                                                               TLFDDEFEKKDRTYPVGEKLRNAFRCSSAKIKAVVFGLLPVLSWLPKYKIKDYIIPDLLG 77
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                                                             TTTDQDIVEKKECSPFRKKLQK
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y 672 ISHGC : : b 579 LSNDE	y 612 SDML <i>i</i> b 519 IGKLF	y 552 AKTVS	y 493 VVFQ7 : : b 468 LVLRC	y 433 VLGAI : : b 408 ILACI	y 373 GCSNE :: b 348 GIAS	y 313 GEIQF b 288 YEIPF	y 258 FALIS :: b 232 ISI	y 198 YLSES : 	y 138 ICLQI : b 114 ARLRI
ISHGGVFEDGSLECKHVFPSIHDAVLFAQANARDV 706 : : : : LSNDENFL-SVVPPSTFFPSI-DSCLISFVHQQSV 611	SDMLASVPPFVTFHTLILDMSGVSFVDLMGIKALAKLSSTYGKIGVKVFLVNIHAQVYND 671 	AKTVSLQELQQDFENAPPTDPNNNQTPANGTSVSYITFSPDSSSPAQSEPPASAEAPGEP 611	VVEQTQERNGYALAQVMDTDIYVNPKTYNRAQDI-QGIKIITYCSPLYFANSEIFRQKVI 551 : : :	VLGALIAVNLKNSLKQLTDÞYYLWRKSKLDCCIWVVSFLSSFFLSLÞYGVAVGVAFSVLV 492 : :: : : : :	GCSNFFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMITMLVLGIYLYPLPKS 432 :: :: : : : : : : : : :	GEIQRGFPTPVSPVVSQWKDMIGTAFSLAIVSYVINLAMGRTLANKHGYDVDSNQEMIAL	FALISGAFLVLVKELNARYMHKIRFPIPTEMIVVVVATAISGGCKMPKKYHMQIV 312 : : :	YLSESFIRGFMTAAGLQILISVLKYIFGLTIPSYTGPGSIVFTFIDICKNLPHTNIASLI 257 : : : : : : : : :	ICLQLAPESKEQVENNATNESYVDTAAMEAERLHVSATLACLTAIIQMGLGEMQEGEVAI 197 : : : : : : : : : :
	671 578	611 518	551 511	492 167	432 107	372 347	312 287	257 231	197 171

Search completed: April 26, 2002, 09:06:43 Job time: $134\ \text{sec}$

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OM protein - protein search, using sw model
                                                                                    GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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April 26, 2002, 09:04:39; Search time 12.77 Seconds (without alignments) 2161.990 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-749-589-2 3869 1 MSQPRPRYYVDRAAYSLTLF.....WDLEQEMFGSMFHAETLTAL 753

Searched: BLOSUM62 Gapop 10.0 , Gapext 0.5 100059 seqs, 36664827 residues

Scoring table:

Total number of hits satisfying chosen parameters:

100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SwissProt_39:*

Database :

SUMMARIES

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1190 974.5 972.9 973.5 984.5 985.5 984.5 863.5 864.5 443.5 443.5 357 357 375.5 375.5 375.5 113.5 113.5 1114.5 1114.5 1113.5	Score
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NU5C_DIGGR	BIO5_YEAST	SECY_METVA	NORM_BACSU	NU5C_GERJA	YHFT_ECOLI	RGT2_YEAST	LCNC_LACLA	BENE_ACICA	NU5M_ALBCO	VMT1_HUMAN	NORM_CAUCR
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digitalis g	saccharomyc	methanococc	bacillus su	gerbera jam	escherichia	saccharomyc	lactococcus	acinetobact	albinaria c	homo sapien	caulobacter

ALIGNMENTS

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Li X.C., Everett L.A., Lalwani A.K., Desmukh D., Friedman T.B.,			Hum. Mol. Genet. 7:1105-1112(1998).	"Molecular analysis of the PDS gene in Pendred Syndrome (sensorineural hearing loss and goitre) ":	mbath R.C.;	Phelps P.D., Luxon L.,	Gausden E.	N)	[5]	Hum. Mol. Genet. 7:1099-1104(1998).	"Two frequent missense mutations in Pendred syndrome.";	,	Stalpers C., Bolder C., Otten B., de Vijlder J.J.M.,	<pre>van Hauwe P., Everett L.A., Coucke P., Scott D.A., Kraft M.L.,</pre>	VARIANTS PDS PRO-236 AND PRO-416.	[4]	protein."; Nat. Genet. 21:440-443/1999).	ed syndrome gene encodes a chloride-iodide transport	NE=9920661/; PubMed=10192399; D.A., Wang R., Kreman T.M., She			Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.	SEQUENCE OF 335-780 FROM N.A.	1	Nat. Genet. 17:411-422(1997).	rendred syndrome is caused by mucacions in a pacacive safphace transporter gene (PDS).":	hy mutations in a nutative	F., Hazani E., Nassir E., Baxevanis A.D., Sheffield V.C.,	ser B., Beck J.C., Idol J.R., Buchs A., I	TISSUE=Thyrold; MEDI.TNF=98061089: PubMed=9398842:	SEQUENCE FROM N.A., AND VARIANT PDS CYS-667.	NCB1_TdX1D=9606;	Primates;	Chordata; Craniata; Vertebrata; E	Homo sapiens (Human).	PENDRIN (SODIUM-INDEPENDENT CHLORIDE/IODIDE TRANSPORTER).	20-AUG-2001 (Rel. 40, Last annotation update)	15-JUL-1999 (Rel. 38, Last sequence update)	15-111-1000 (B) 38 (100+0d)	3	HUMAN	

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Hum. Genet. 104:188-192(1999).

-I- FUNCTION: SODIUM-INDEPENDENT TRANSPORTER OF CHLORIDE AND IODIDE.

-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

-I- TISSUE SPECIFICITY: HIGH EXPRESSION IN ADULT THYROID, LOWER EXPRESSION IN ADULT AND FETAL KIDNEY, AND FETAL BRAIN.

NOT EXPRESSION IN ADULT AND FETAL KIDNEY, AND FETAL BRAIN.

NOT EXPRESSED IN OTHER TISSUES.

-I- DISSASE: DEFECTS IN PDS ARE A CAUSE OF PENDRED SYNDROME, AN AUTOSOMAL RECESSIVE DISORDER CHARACTERIZED BY CONGENITAL SENSORIBURAL HEARING LOSS COMBINED WITH THYROID GOTTRE. THE DISORDER MAY ACCOUNT FOR UP TO 10% OF THE CASES OF HEREDITARY DEARNESS. THE DEAFNESS IS MOST OFTEN ASSOCIATED WITH A MONDINI COCHLEAR DEFECT.
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InterPro; IPR001902; Sulfate_transp.
Pfam; PF01740; STAS; 1.
Pfam; PF00916; Sulfate_transp; 1.
PROSITE; PS01130; SULFATE_TRANSP; 1.
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EMBL; AC002467; AAB88773.1;
MIM; 274600; -
MIM; 603945; -
MIM; 600791; -
                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Usami S., Abe S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANTS EVA VAL-209; GLU-369; VAL-372; MET-721 AND ARG-723 MEDLINE-99204606; Pubmed-10190331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Non-syndromic hearing loss associated aqueduct is caused by PDS mutations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISEASE: DEFECTS IN PDS ARE THE CAUSE OF ENLARGED VESTIBULAR AQUEDUCT SYNDROME (EVA); A COMMON FORM OF INNER EAR ABNORMALITY ASSOCIATED WITH FLUCTURATING AND SOMETIMES PROGRESSIVE SENSORINEURAL HEARING LOSS AND DISEQUILIBRIUM SYMPTOMS. DISEASE: DEFECTS IN PDS ARE THE CAUSE OF AUTOSOMAL RECESSIVE DEAFNESS TYPE 4 (DFNB4).

SIMILARITY: BELONGS TO THE SULFATE PERMEASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DATABASE:
NOTE-Gene
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 page;
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Disease mutation; Deafness; Glycoprotein
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6 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
7 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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FY TRANSFER 553 573 11 (FOTENTIAL). FY CARROIND 415 415 07-14KED (POTENTIAL). FY CARROIND 416 416 7-2 P (IN PDS). FY VARIANT 369 369 K-FTG-WARLOO744. FY VARIANT 372 372 A-P (IN PDS). FY VARIANT 416 416 7-2 P (IN PDS). FY VARIAN	EAPGEPSDMLASVPPFVTFHTLILDMSGVSFVDL	SEPPASA	DSSSPAQS	FSP	589	Qy	
TRANSSEM 633 673 CARBONYD 415 415 CARRONYD 415 415 VARIANT 209 209 6 -> V (IN EVA). VARIANT 236 236	SLQELQQDFENAPPTDPNNNQTPANGTSVS 	FDAI	KVIAKTV KCIKSTV	GF -	σ <u>4</u>	Фу	
TRANSEM	YALAQVMDTDIYVNPKTYNRAQDIQGIKIITYCSPL 	FRN : FPS	SVLVVV GLLTVV	G - 6	0 &	Дb	
TRANSSEM 6.53 6.73 11 (POTENTIAL). CARBOHYD 415 415 0-LINKED (POTENTIAL). VARIANT 209 209 6 -V (IN EVA). VARIANT 369 369 K->E (IN EVA). VARIANT 369 369 K->E (IN EVA). VARIANT 369 369 K->E (IN EVA). VARIANT 372 372 A->V (IN EVA). VARIANT 416 416 F->C (IN EVA). VARIANT 721 721 F->M (IN EVA). VARIANT 722 723 F->C (IN EVA). VARIANT 723 723 F->C (IN EVA). VARIANT 723 723 F->M (IN EVA). VARIANT 721 721 F->M (IN EVA). VARIANT 722 723 F->M (IN EVA). VARIANT 723 723 F->M (IN EVA). VARIANT 723 723 F->M (IN EVA). VARIANT 721 721 F->M (IN EVA). VARIANT 722 723 F->M (IN EVA). VARIANT 723 723 F->M (IN EVA). VARIANT 722 723 F->M (IN EVA). VARIANT 723 723 F->M (IN EVA). VARIANT 721 721 F->M (IN EVA). VARIANT 722 F->M (IN EVA). VARIANT 723 723 F->M (IN EVA). VARIANT 721 721 F->M (IN EVA). VARIANT 722 F->M (IN EVA). VARIANT 723 723 F->M (IN EVA). VARIANT 721 F->M (IN EVA). VARIANT 722 F->M (IN EVA). VARIANT 723 F->M (IN EVA). VARIANT 1049 F->M (IN EVA). VARIA	DPYYLWRKSKLDCCIWVVSFLSSFFLSLF : : DIPRLWRQNKIDAVIWVFTCIVSIILGLI	LIA.	LPKSVLG LQKSVLA	Ε Κ	4 2	Qу	
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TRANSHEM 653 673 11 (POTENTIAL). DOMAIN 644 780 EXTRACELLULAR (POTENTIAL). CARBOHYD 415 415 0-LINKED (POTENTIAL). VARIANT 209 209 6 -> V (IN EWA). VARIANT 236 236 L -> P (IN PDS). VARIANT 369 369 K -> E (IN EWA). VARIANT 372 372 A -> V (IN EWA). VARIANT 372 372 A -> V (IN EWA). VARIANT 384 384 E -> G (IN PDS). VARIANT 416 416 T -> P (IN PDS). VARIANT 497 497 G -> S (IN DENS). VARIANT 667 667 FTIG=VAR_007444. VARIANT 667 667 FTIG=VAR_007445. VARIANT 721 721 T -> P (IN PDS). VARIANT 721 721 T -> M (IN EWA). VARIANT 723 723 H -> R (IN EWA). VARIANT 723 723 H -> R (IN EWA). VARIANT 723 723 H -> R (IN EWA). VARIANT 721 721 T -> M (IN EWA). VARIANT 723 723 H -> R (IN EWA). VARIANT 724 T -> M (IN EWA). VARIANT 725 725 MW; JAREFSD720B155CEO CRC64; Matches 256; Conservative 146; Mismatches 283; Indels 3	-DRTYPVGEKLRNAFRCSSAKIKAVVFGLLPVLS	DDEF	- 10	YVVDI	æ	Q	
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RESULT 2
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Hoeglund P., Haila S., Socha J., Tomas
Karjalainen Lindsberg M.-L., Airola K
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permease II and a putative human tumour suppressor.";
Trends Biochem. Sci. 19:19-19(1994).
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EMBL; L02785; AAA58443.1; MIM; 126650; -. MIM; 214700; -.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                  or send an
                                                               entities
                                                                                                                                                                                                                                                                                                         Hoeglund P., Haila S., Gustavson K.-H., Taipale M.,
Popinska K., Holmberg C., Socha J., de la Chapelle A
                                                                                                                                                                                                                                                                                                                                                                                      congenital chloride diarrhoea.";
                                                                                                                                                                                                                                                                                                                                                                                               de la Chapelle A., Kere J.;
"Mutations of the Down-regulated
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                                                                                                   European Bioinformatics Institute.
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                                                                                                              SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EM
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                                               non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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InterPro; IPR002645; STAS.
InterPro; IPR001902; Sulfate_transp.
Pfam; PF01740; STAS; 1.
Pfam; PF00916; Sulfate_transp; 1.
PROSITE; PS01130; SULFATE_TRANSP; 1.
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J. Biol. Chem. 273:12307-12315(1998).
-i-FUNCTION: SULFATE TRANSPORTER. MA
BONE FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Osteosarcoma;
MEDLINE=98241598; PubMed=9575183;
Satoh H., Susaki M., Shukunami C., I
Satoh H., Susaki M., Shukunami C., I
"Functional analysis of diastrophic
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15-JUL-1999 (Rel. 38, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SULFATE TRANSPORTER (DIASTROPHIC DYSPLASIA PROTEIN HOMOLOG)
SLC26A2 OR DTDST.
                                                                                                                                     TRANSMEM
                                                                                                                                                                                          Transport;
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SIMILARITY: BELONGS TO THE SULFATE PERMEASE FAMILY.
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CYTOPLASMIC (POTENTIAL).
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POTENTIAL.
EXTRACELLULAR
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Sciurognathi; Muridae; Murinae; Rat
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                                                                                         GSLECKH-----VFPSIHDAVLFAQANARD
                                                                                                                                                                FVTFHTLILDMSGVSFVDLMGIKALAKLSSTYGKIGVKVFLVNIHAQVYNDISHGGVFED
                                                                                                                                                                                                                                            QQDFENAPPTDPNNNQTPANGTSVSYITFSPDSSSPAQSEPPASAEAPGEPSDMLASVPP
                                                                                                                                                                                                                                                                                                                                                                              NLKNSLKQLTDPYYLWRKSKLDCCIWVVSFLSSFFLSLPYGVAVGVAFSVLVVVFQTQFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGEKLRNAFRCSSAKIKAVVFGLLPVLSWLPKYKIKDYIIPDLLGGLSGGSIQVPQGMAF
                                                                                                                                                                                                         KAAWKKAAKRKLKEET------VTFHGD-
                                                                                                                                                                                                                                                                                 KISLLGLEEESEIFESISTYKNLRSKSGIKVFRFIAPLYYINKECFKSALYKKTLNPVLV
                                                                                                                                                                                                                                                                                                                    NGYALAQVMDTDIYVNPKTYNRAQDIQGIKIITYCSPLYFANSEIFRQKVIAKTVSLQEL
                                                                                                                                                                                                                                                                                                                                                        NLRGALLKERDLPKMWRLSRMDTVIWFVTMLSSALLSTEIGLLVGVCFSMFCVILRTQMP
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                                                                                                                             -LELHTVVIDCSAIQFLDTAGIHTLKEVRRDYEAIGIQVLLAQCNPSVRDSLAKGEY---
                                                                                                                                                                                                                                                                                                                                                                                                                                  FFHCITTSAALAKTLVKESTGCQTQLSAIVTSLVLLLVLLLIAPLFYSLQKCVLGVITIV
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19; Conservative
                                                        -CKKEEENLLFYSLSEAVAFAEESQKE
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N-LINKED (GLCNAC. . .) (P
CC539F66D478C8DA CRC64;
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CYTOPLASMIC (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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No. 1.2
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01-OCT-1996
20-AUG-2001
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SULFATE TRANSPORTER (DIASTROPHIC DYSPLASIA PROTEIN)
SLC26A2 OR DTDST OR DTD.
HOMO Saniene /u----
                                                                                               entities
or send a
EMBL; U14528; AAA70081.1; MIM; 222600; -. MIM; 600972; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dysplasia sulfate-transporter gene (DTDST): series involving three chondrodysplasias."; Am. J. Hum. Genet. 58:255-262(1996).
i- FUNCTION: SULFATE TRANSPORTER. MAY PLAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Achodrogenesis type IB is caused by mutations in dysplasia sulphate transporter gene.";
Nat. Genet. 12:100-102(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mapping.";
Cell 78:1073-1087(1994).
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MEDLLINE=95007757; PubMed=7923357;
Haestbacka J., de la Chapelle A., Mahtani M.M., Clines G.,
Haestbacka J., de la Chapelle A., Mahtani M.M., Trivedi B.,
Reeve Daly M.P., Daly M., Hamilton B.A., Kusumi K., Trivedi B.,
Weaver A., Coloma A., Lovett M., Buckler A., Kaitila I., Lander E.S.
"The diastrophic dysplasia gene encodes a novel sulfate transporter:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS AO-II GLU-255; TRP-279 A
MEDLINE-96152121; PubMed-8571951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-96122050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               positional cloning by fine-structure
mapping.";
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                                                                                                                         modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                 use
                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lander E.S.;
"Atelosteogenesis type II is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haestbacka J., Superti-Furga A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superti-Furga A., Haestbacka J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS ACG-IB VAL-340 DEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BONE FORMATION.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
DISCASE: DEFECTS IN DTDST ARE THE CAUSE OF DIASTROPH (DTD), AN AUTOSOMAL RECESSIVE DISEASE CHARACTERIZED
                                                                                                                                                                                                                                                                                                                                                     DISEASE: DEFECTS IN DYDST ARE THE CAUSE OF ATELOSTEOGENESIS II (AO-II), ALSO KNOWN AS NEONATIAL OSSEOUS DYSPLASTA I, WHICH CHARACTERIZED BY SEVERELY SHORTENED LIMES, SMALL CHEST, SCOLL CLUB FOOT OF THE EQUINOVARUS TYPE (TALIPES EQUINOVARUS), ABBUTHUMBS AND GREAT TOES, AND CLEFT PALTENTS DIE OF RESPIRATORY INSUFFICIENCY SHORTLY AFTER BIRTH BECAUSE OF THE COLLAPSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE SECOLAPSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE SECOLAPSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE SECOLAPSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE SECOLAPSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE SECOLAPSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE SECOLAPSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE SECOLAPSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE SECOLAPSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE SECOLAPSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE SECOLAPSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE SECOLAPSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE SECOLAPSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE SECOLAPSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE SECOLAPSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE SECOLAPSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE SECOLAPSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE SECOLAPSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE SECOLAPSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE SECOLAPSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE SECOLAPSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE SECOLAPSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE SECOLAPSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE SECOLAPSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE SECOLAPSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE SECOLAPSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE MAIR AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE PULMONARY AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE PU
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DISEASE: DEFECTS IN DTDST ARE THE CAUSE OF ACHONDRODENESIS TYPE (ACG-IB). ACG-IB IS A RECESSIVELY INHERITED CHONDRODYSPLASIA CHARACTERIZED BY EXTREMELY POOR SKELETAL DEVELOPMENT AND PERINATERS.
                                                                                                                                                                                                         European
                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE SULFATE PERMEASE FAMILY.
                                                                                                                                                                                                                                                                                                                                     RIB
                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the BMBD outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                            s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -Furga A., Haestbacka J., Wilcox W.R., (Harten H.J., Rossi A., Blau N., Rimoin
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SULFATE TRANSPORTER. MAY PLAY A ROLE IN
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Pfam; PF00916; Sulfate_transp;
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InterPro; IPR001902;
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138; Mismatches
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G -> E (IN AO-II).
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G -> V (IN ACG-IB).
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R -> W (IN AO-II).
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SEQUENCE FROM N.A.
MEDIINE-98036067; PubMed-9370300;
Kobayashi T., Sugimoto T., Saijoh K., Fukase M., Chihara K.;
Kobayashi T., Sugimoto T., Saijoh K., Fukase M., Chihara K.;
Foloning of mouse diastrophic dysplasia sulfate transporter gene
Foloning of mouse diastrophic dysplasia sulfate morphogenetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DTD_MOUSE
Q62273;
Q1-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SULFATE TRANSPORTER (DIASTROPHIC DYSPLASIA PROTEIN HOMOLOG)
SLC26A2 OR DTDST OR DTD.
                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
             EMBL; D42049; BAA07650.1; -. MGD; MGI:892977; S1c26a2.
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MGD; MGI:892977
InterPro; IPR00
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                                                                                                                                                                                                             TISSUE SPECIFICITY: OSTEOBLASTIC CELLS.
                                                                                                                                                                                                                           SUBCELLULAR LOCATION: INTEGRAL MISSUE SPECIFICITY: DISTRIBUTED
                                                                                                                                                                                                                                                                        FUNCTION: SULFATE TRANSPORTER.
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Pfam; PF00916; Sulfate_transp;
PROSITE; PS01130; SULFATE_TRAN
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TPVSPVVSQWKDMIGTAFSLAIVSYVINLAMGRTLANKHGYDVDSNQEMIALGCSNFFGS
                             NLRGALLKFRDLPKMWRLSRMDTVIWFVTMLSSALLSTEIGLLVGVCFSMFCVILRTQKP
                                             NLKNSLKQLTDPYYLWRKSKLDCCIWVVSFLSSFFLSLPYGVAVGVAFSVLVVVFQTQFR
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                                                                 FFHCITTSAALAKTLVKESTGCQTQLSAIVTALVLLLVLLVIAPLFYSLQKCVLGVITIV
                                                                                  FFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMITMLVLGIYLYPLPKSVLGALIAV
                                                                                                     PPKAPDWSLIPNVAVDATAISIIGFAITVSLSEMFAKKHGYTVKANQEMYAIGFCNIIPS
                                                                                                                                           LCLLVLVPSKELNEHFKDKLKAPIPVELIVVVAATLASHFGKLNGNYNSSIAGHIPTGFM
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137; Mismatches 274;
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
SULFATE ANION TRANSPORTER 1 (CANALICULAR SULFATE TRANSPORTER)
                                                    TRANSMEM
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system of rat hepatocytes.";
J. Biol. Chem. 269:3017-3021(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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           CARBOHYD
                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a coefficient the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-94132077; PubMed-8300633;
                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                               EMBL; L23413; AAA17545.1; -.
                                                                                                                                                                                                                                                                               the European Bioinformatics Institute.
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InterPro; IPR001902; Sulfate_transp.
Pfam; PF01740; STAS; 1.
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                                                                                                                                                                                                                                                                                                                                           NOT SUCCINATE AS A CO-SUBSTRATE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
TISSUE SPECIFICITY: LIVER, KIDNEY. LESS
                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE SULFATE PERMEASE FAMILY.
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Sciurognathi;
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(GLCNAC. . GLCNAC. .
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                                     NCBI_TaxID=6239;
                                                         Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                Caenorhabditis elegans
           STRAIN-BRISTOL N2;
                        SEQUENCE FROM N.A
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                                                            Caenorhabditis.
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Pred.
                                                                      Chromadorea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted [2]
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InterPro; IPR001902; Sulfa
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KRYKYKINHGQELYALGFVGVLSSFFPVFPVTSGFARSVVGAAVGGSTQLTCLFSSLALL
                      NKHGYDVDSNQEMIALGCSNFFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVM
                                                                                                                     VFTFIDICKNLPHTNIASLIFALISGAFLVLVKELNARYMHK-IRFPIPTEMIVVVVATA
                                                                                                                                                                                                                                                                                                                QKLR--YACSPSKCIHSLLSFLPIITWLPKYDWSHSFFGDLSGGLTMAVFSVPQGIALAS
                                                                                                                                                                                                                                                                                                                                       EKLRNAFRCSSAKIKAVVFGLLPVLSWLPKYKIKDYIIPDLLGGLSGGSIQVPQGMAFAL 94
                                                                        ISGGCKMPKKYHMQIVGEIQRGFPTPVSPVVSQWKDMIGTAFSLAIVSYVINLAMGRTLA
                                                                                                     YYRIWDLVENLDNVHIPTVCISLSSFLFLVFGKEYLAPWLNSAFNYPVPFELVLLT----
                                                                                                                                                      FLAGVIQVFMGVFRLQYLTSLFSEQVMSGFVVGGGIHVFFAQIGNMLGIELPRRSGPGYL
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                                                                                                                                                                                                                           ------PESKFQVFNNAT-----NE-SYVDTAAME------AERLHVSATLA
                                                                                                                                                                                                                                                           ITGVPPVYGLYTAIFPSFLYIFFGTSKHNALGGFAVLSLMTHGAIEKVMLRTATSYNATA
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PF00916; Sulfate_transp;
TE; PS01130; SULFATE_TRAN
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Proc. Natl. Acad. Sci. U.S.A. 92:9373-9377(1995).

-I- FUNCTION: HIGH-AFFINITY H+/SULFATE COTRANSPORTER THAT MEDIATES

UPTAKE OF SULFATE BY PLANT ROOTS FROM LOW CONCENTRATIONS OF

SULFATE IN THE SOIL SOLUTION.
                                                                                                                                                                                                                                                                                                        This
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MEDLINE=96016171; PubMed=7568135;
Smith F.W., Ealing P.M., Hawkesford M.J.,
"Plant members of a family of sulfate tran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids I; Fabales; Fabaceae; Papilionoideae; Aeschynomeneae;
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                                                                                                              Transmembrane;
                                                                                                                                                                 InterPro; IPR002645; InterPro; IPR001902;
                                                                                                                                                                                              EMBL; X82256; CAA57711.1;
                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinf
the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
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P53392;
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                                                                                                                     PF00140; STAS; 1.
PF00916; Sulfate_transp; 1.
PF00916; Sulfate_TRANSP; 1
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AFFINITY SULPHATE TRANSPORTER 1.
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MEDLINE=96016171; PubMed=7568135;
Smith F.W., Ealing P.M., Hawkesford M.J., Clarkson
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                                                                                                                            GFVAIYLSESFIRGFMTAAGLQILISVLKYIFGLTIPSYTGPGSIVFTFIDICKNLPH-T
                                                                                                                                                                    LLLGTL---LSNE----ISNTKSHDYL-----
                                                                                                                                                                                                                              GDFIAGLTIASLCIPQDLAYAKLANLDPWYGLYSSFVAPLVYAFMGTSRDIAIGPVAVVS
                                                                                                                                                                                                                                                                                                                 TLFDDEFEKKDRTY----PVGE-KLRNAFRCSSAKIKAVVFGLLPVLSWLPKYKIKDYII 72
VKHIKSGVNPSSANEIFFHGK-YLGAGVRVGVVAGLVALTEAIAIGRTFAAMKDYALDGN
                         VGEIQRGF-PTPVSPVVSQWKDMIGTAFSLAIVSYVINL----AMGRTLANKHGYDVDSN
                                                                                 NIASLIFALISGAFLVLVKELNARYMHKIRFPIPTEMIVVVVATAISGGCKMPKKYHMQI
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                                                       NWETILIGLSFLIFLLITKYIAKKNKKLFWVSAISPMISVIVSTFFVYITRADKR-GVSI
                                                                                                              GFLIDFLSHAAIVGFMAGAAITIGLQQLKGLLGISNNNFTKKTDIISVMRSVWTHVHHGW
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PROSITE; PS01130; SULFATE_TRANSP; 1.
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STRAIN-CV. VERANO; TISSUE-ROOT;
MEDLINE-96016171; PubMed-7588135;
Smith F.W., Ealing P.M., Hawkesford M.J.,
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Proc. Natl.
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EUNCTION: LOW-AFFINITY H+/SULFATE COTRANSPORTER WHICH
INVOLVED IN THE INTERNAL TRANSPORT COTRATE BETWEEN
SUBCELLULAR COMPARTMENTS WITHIN THE PLANT.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTEN
SIMILARITY: BELONGS TO THE SULFATE PERMEASE FAMILY.
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Schizosaccharomyces pombe (Fission yeast).
Schizosaccharomycetes;
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
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Badcock K., Bowman S., Churcher C.M., Pearson
Walsh S.V., Barrell B.G.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ
-!- FUNCTION: POSSIBLE SULFATE TRANSPORTER.
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01-OCT-1996 (Rel. 34, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
PUTATIVE SULFATE TRANSPORTER YPR003C.
                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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30; SULFATE_TRANSP; FALSE_NEG
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Pred. No. 9e-22;
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EMBL; 273264; CAA97653.1;
EMBL; 273265; CAA97655.1;
EMBL; U53876; AAB67550.1;
SGD; S0004082; SUL2.
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15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
15-UUL-1999 (Rel. 38, Last annotation update)
SULFATE PERMEASE 2 (HIGH-AFFINITY SULFATE TRANSPORTER 2).
SUL2 OR SEL2 OR YLR092W OR L9449.1.
Succharomyces cerevisiae (Baker's yeast).
Saccharomyces cerevisiae (Baker's Saccharomycotina; Saccharomycetes;
Saccharomyces.
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Johnston M., Andrews S., Brinkman R., Cooper J., Ding H.,
Favello A., Fulton L., Gattung S., Greco T., Kirsten J., K
Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.
Johnston L., Langston Y., Latreille P., Le T., Mardis E.,
Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles
Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P.
Wilson R., Waterston R.;
                          TRANSMEM SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in Saccharomyces cerevisiae.";
Genetics 145:627-635(1997).
-!- FUNCTION: HIGH AFFINITY UPTAKE OF SULFATE INTO THE CELL.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE SULFATE PERMEASE FAMILY.
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"Molecular characterization
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Benes V., Rechmann S
Submitted (MAY-1996)
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InterPro; IPR001902; St
Pfam; PF01740; STAS; 1.
Pfam; PF00916; Sulfate_
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STRAIN=INVSC1;
MEDLINE=95342164; PubMed=7616962;
Smith F.W., Hawkesford M.J., Prosser I.M., Clarkson D.
Smith F.W., Hawkesford M.J., Prosser I.M., Clarkson D.
"Isolation of a cDNA from Saccharomyces cerevisiae tha
high affinity sulphate transporter at the plasma membr
Mol. Gen. Genet. 247:709-715(1995).
                                                                                                                                                                                                 01-OCT-1994 (Rel. 30, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
SULFATE PERWEASE 1 (HIGH-AFFINITY SULFATE TRANSPORTER
SUL1 OR SFP OR YBR294W OR YBR2110.
                                                                                                                                                                                                                                                                                                 SUL1
                                                                                                                                                                                                                                                                                                                    _YEAST
                                                                                                                                                      Saccharomycetales;
                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
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01-OCT-1994
                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                      Saccharomycetaceae;
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8; Mismatches
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                                                                                                                                                        Saccharomyces
                                           cerevisiae that encodes
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                          plasma membrane.";
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PIIKWFPHYNF-TWGYADLVAGITVGCVLVPQSMSYAQIASLSPEYGLYSSFIGAFIYSL PVLSWLPKYKIKDYIIPDLLGGLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFF VNSSKOKFGVTKNELSDVLYDSIPAYEESTVTLKEYYDHSIKNNLTAKSA--GSYLVSLF

Query Match Best Local Matches

Similarity

9.7%;

Score Pred.

Conservative

156;

Mismatches

Indels

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Genetics 145:627-635(1997).
-!- FUNCTION: HIGH AFFINITY UPTAKE
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Submitted (MAR-1998)
                                                                                                              TRANSMEM TRANSMEM
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SGD;
                                                                                                                                                                                                                           EMBL; Z36163; CAA85259.1;
EMBL; X82013; CAA57540.1;
EMBL; Z35134; CAA84506.1;
PIR; S46176; S46176.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jin Y.H., Jang Y.K., Kim M.J., Park S.D.;
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Fritz C., Hol
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SEQUENCE FROM N.A.
                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
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                                                                                                                                                        Transport;
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IPR001902; Sulfate_transp
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                                                                                                                                                                           _transp;
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01-FEB-1995 (Rel. 31, I
01-NOV-1995 (Rel. 32, I
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  genes
                                                                                                       SEQUENCE FROM N.A.
STRAIN-CV. AKISENGOKU;
                                                                                                                                                                                                                                                                                            EARLY NODULIN
Glycine max (S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOYBN
                           "Isolation
                                                   Kouchi H., Hata S.;
                                                                               MEDLINE=93241143; PubMed=7683079;
                                                                                                                                                                                    NCBI_TaxID=3847;
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Sandal N.N., Marcker A. soybean nodulin, Neurospora crassa sulphate
"Similarities between a soybean nodulin, Neurospora crassa sulphate
"Similarities between a soybean nodulin, Neurospora;";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (Second or send an email to license@isb-sib.ch).
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PPO; IPR001902;
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                                                                                     FGIDNENNKTDLESVVKSLWTSEKNQSAWHPYNLIIGESELCEILETRELGKRNKKLMWL
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Search completed: April 26, 2002, 09:07:03 Job time: 144 sec	442 KAREIWKVDKMDFLACTGAFLGVLFASVEIGLAIG 476	451 DPYYLWRKSKLDCCIWVVSFLSSFFLSLPYGVAVG 485	383 LSRTAVNYNAGSETMVSIIVMALTVLMSLKFLTGLLYFTPKAILAAII-LSAVPGLIDLN 441	391 LSVTLAVDGAGGKSQVASLCVSLVVMITMLVLGIYLYPLPKSVLGALIAVNLKNSLKQLT 450	325LIRIGLTIAIISLTGSIAVGRSFASLKGHSIDPNREVVSLGIMNIVGSLTSCYIASGS 382

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A; Residues: 1-764 < RES>
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probable sulfate	C64867	N	550	6.0	230.5	5
hypothetical prote	D85700	N	550	6.0	230.5	4
sulfate permease	D82303	2	548	6.2	238	ω
integral membrane	S76624	2	556	6.4	249.5	2
sulfate permease	A37956	ده	781	6.5	250	41
sulfate permease	A82505		553	7.4	286.5	0
probable sulfa	T41306		667	8.1	313	39
probable sulfate	_	2	517	8.2	315.5	8
hypothetical p			560	9.4	365.5	37
sulfate permease			592	9.6	372	36
sulfate transpor			485	9.7	375.5	5
sulfate transpor	S46176		859	9.7	376	34
high affinity sul	S74633		566	10.0	386	ω
probable membrane	S64926		893	10.5	405	Ñ
probable membrane	S52816	2	754	11.3	437	~
protein F28K19.22	D96809		719	11.4	441.5	õ

ALIGNMENTS

A;Gene: GDB:DRA
A;Cross references: GDB:138165; OMIM:126650
A;Map position: 7q22-7q31.1
C;Superfamily: sulfate transport protein
C;Keywords: tumor suppressor C;Accession: A47456

R;Schweinfest, C.W.; Henderson, K.W.; Suster, S.; Kondoh, N.; Papas, T.S.

Proc. Natl. Acad. Sci. U.S.A. 90, 4166-4170, 1993

A;Title: Identification of a colon mucosa gene that is down-regulated in colon adenom A;Reference number: A47456; MUID:93248250

A;Accession: A47456 down-regulated in adenoma (DRA) - human
C;Species: Homo sapiens (man)
C;Date: 10-May-1996 #sequence_revision 10-May-1996 #text_change 26-Aug-1999 A;Cross-references: GB:L02785; NID:g291963; PID:g291964 C;Genetics: A;Status: preliminary; translated from GB/EMBL/DDBJ 359 7 RYVVDRAAYSLTLFDDEFEKKDRTYPVG-EKLRNAFRCSSAKIKAVVFGLLPVLSWLPKY 65 LTAIIQMGLGFMQFGFVAIYLSESFIRGFMTAAGLQILISVLKYIFGLTIPSYTGPGSIV 238 GGCKMPKKYHMQIVGEIQRGFPTPVSPVVSQWKDMIGTAFSLAIVSYVINLAMGRTLANK KVLYSVESQIEKTNIADLVTALIVLLVVSIVKEINQRFKDKLPVPIPIEFIMTVIAAGVS GPFPILSMMVGLAVSGAVSKAVPDRNATTLGLPNNSNNSSLLDD---ERVRVAAAASVTV 184 GTFAVISILVG----NICLQLAPESKFQVF---NNATNESYVDTAAMEAERLHVSATLAC 178 RLKEWLLSDIVSGISTGIVAVLQGLAFALLVDIPPVYGLYASFFPAIIYLFFGTSRHISV 127 KIKDYIIPDLLGGLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLGGVHQMVP 125 QYIVARPVYSTNAFEENHKKTGRHHKTFLDHLKVCCSCSPQKAKRIVLSLFPIASWLPAY 67 HGYDVDSNQEMIALGCSNFFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMIT YGCDFKNRFKVAVVGDMNPGFQPPITPDVETFQNTVGDCFGIAMVAFAVAFSVASVYSLK FTF IDICKNLPHTNIASLIFALISGAFLYLVKELNARYMHKIRFPIPTEMIVVVVATAIS LSGIIQLAFGILRIGFVVIYLSESLISGFTTAAAVHVLVSQLKFIFQLTVPSHTDPVSIF 28.9%; Score 1120; 34.0%; Pred. No. 2 142; Mismatches DB 2; 2.9e-78; Length 764; Indels 68; Gaps 418 364 298 304 244 11;

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Cell 78, 1073-1087, 1994

A; Fittle: The diastrophic dysplasia gene encodes a nov A; Reference number: A54808; MUID:95007757

A; Accession: A54808

A; Status: not compared with conceptual translation A; Molecule type: mRNA
A; Residues: 1-739 < HAE>
A; Cross-references: GB:U14528
C; Genetics:
A; Gene: GDB:DTD; DTDST
A; Cross-references: GDB:125421; OMIM:222600
A; Map position: 5q32-5q33.1
C; Superfamily: sulfate transport protein
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A54808
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-May-1999
C; Accession: A54808
R; Haestbacka, J; de la Chapelle, A.; Mahtani, M.M.; Clines, G.; Reeve-Daly der, E.S.
Cell 78, 1073-1087, 1994
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LTIPSYTGPGSIVFTFIDICKNLPHTNIASLIFALISGAFLVLVKELNARYMHKIRFPIP
                                        ---AIMVGSTVTFIAGVYQVAMGFFQVGFVSVYLSDALLSGFVTGASFTILTSQAKYLLG
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RESULT 3
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sulfate transporter, canalicular - rat
sulfate transporter, canalicular - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jan-1995 #sequence_revision 20-Jan-1995 #text_change 24-Sep-1999.
C;Accession: A49994
R;Bissig, M.; Hagenbuch, B.; Stieger, B.; Koller, T.; Meier, P.J.
J. Biol. Chem. 269, 3017-3021, 1994
A;Title: Functional expression cloning of the canalicular sulfate transport system
. Paference number: A49994; MUID:94132077
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:L23413; NID:9431452; PIDN:AAA17545.1; PID:9431453 C;Superfamily: sulfate transport protein C;Keywords: glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-703 <BIS>
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Best Local
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                                                                                                                                                                                                                                                                   36 KLRNAFRCSSAKIKAVVFGLLPVLSWLPKYKIKDYIIPDLLGGLSGGSIQVPQGMAFALL 95
SFIRGEMTAAGLQILISVLKYIFGLTIPSYTGPGSIVETFIDICKNLPHTNIASLIFALI
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                                                                                                                                                                          ANLPAVNGLYSSFFPLLTYFFLGGVHQMVPGTFAVISILVGNIC---LQLA-----
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                                                                                     -PESKFQVFNN-ATNESYVDTAAMEAERLHVSATLACLTAIIQMGLGFMQFGFVAIYLSE
                                                                                                                                     AGLQPIYSLYTSFFANLIYFLMGTSRHVNVGIFSLLCLMVGQVVDRELQLAGFDPSQDSL
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Pred. No. le-57;
3; Mismatches 3
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PLLDGFAMGASVTILTSQAKHLLGVRIPRHQGLGMVIHTWLSLLQNVGQANLCDVVTSAV

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A; Bolecule type: DNA
A; Molecule type: L-611 <WIL>
A; Residues: 1-611 <WIL>
A; Cross-references: EMBL: Z70757; PIDN: CAA94798.1; GSPDB: GN00023; CESP: ZK287.
                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: clone C; Genetics: A; Gene: CESP: ZK287.2
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R; McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein ZK287.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
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A; Introns: 3/3; 102/1; 438/3
C; Superfamily: sulfate trans
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 YLSESFIRGEMTAAGLQILISVLKYIFGLTIPSYTGPGSIVFTFIDICKNLPHTNIASLI 257
                                     ARLRLAPD -- IPISNSSDINPSVYPLGEYVDPLVFTSALTLLVGVVQIIMGILRLGFLTT
                                                                                                               GLTVGIMHVPQGMAYASLAGVPPVYGMYSSFFASTIYMFFGTARHISIGVFAVASMMVGA 113
                                                                                                                                                                                                                            TLFDDEFEKKDRTYPVGEKLRNAFRCSSAKIKAVVFGLLPVLSWLPKYKIKDYIIPDLLG 77
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                                                                       ICLQLAPESKFQVFNNATNESYVDTAAMEAERLHVSATLACLTAIIQMGLGFMQFGFVAI 197
                                                                                                                                                  GLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLGGVHQMVPGTFAVISILVGN 137
                                                                                                                                                                                        TTTDQDIVEKKECSPFRKKLQK------YIPILEWLPNYQWKDHFHGDVIA 53
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197; Conser
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Pred. No. 3e-52;
8; Mismatches 2
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A;Introns: 48/3; 128/1; 165/1; 220/3; 407/3; 471/3; 503/3; 539/2; C;Superfamily: sulfate transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-749 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: clone K12G11
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:Z81570; PIDN:CAB04606.1; GSPDB:GN00023; CESP:K12G11.1
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TSLFPPLIYMLFGTSRHASLGTFAVVSLMTGLSVEKLAAPTDYD--PSSFNETDIDLVKL
                                   SSFFPLLTYFFLGGVHQMVPGTFAVISILVGNICLQLAPESKFQVFNNATNESYVDTAAM 165
                                                                                         --IKAVVFGLLPVLSWLPKYKIKDYIIPDLLGGLSGGSIQVPQGMAFALLANLPAVNGLY 105
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                                                                       FALKLFIFDLIPILKWFPEYKWKTDLSLDIIGGITVGVMQVPQGIAYALLAKQPAINGLY 144
                                                                                                                                               SEPNKRRVSFVQRGAMNQAQFDEKF---DYNKP---HLENELKKQAKKFVRRFYEPFTSF
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28.2%;
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                                                                                                                                                                                                                       ; Score 776.5; 1
; Pred. No. 8.9e
142; Mismatches
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                                                                                                                                                                                                                                           8.9e-52;
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R; Kershaw, J.

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A;Introns: 26/3; 55/2;
C;Superfamily: sulfate
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A;Molecule type: DNA
A;Residues: 1-700 <\script{VIL}\)
A;Cross-references: EMBL:Z81570; PIDN:CAB04607.1; G
A;Experimental source: clone K12G11
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                                                                                                                       RAAYSLTLFDDEFEKKDRTYPVGEKLRNAFRCSS-----AKIKAVVFGLLPVLSWL 62
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                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                   107/1; 197/3; 253/3; transport protein
                                                                                                                                                                                                               19.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Library, November
                                                                                                                                                                            98; Score 768; DB 2; L6
38; Pred. No. 3.7e-51;
141; Mismatches 322;
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                                                                                                                                                                                                                                                                                                                                                                  516/2;
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                                                                                                                                                                       LFHNVECFK-KCIEKVYDEWKKSSEF------NFVKEPNAGKGSKFTFEGMHRIAPI
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                                                                                                                                          SEPPASAEAPGEPSDMLASVPPFVTFHTLILDMSGVSFVDLMGIKALAKLSSTYGKIGVK
                                                                                                                                                                                                                               SEGLLIAIFFALFTTILREQYPKWHLLANVKDTDEFSDTQQYQETIFYKGICIFKFDAPL
                                                                                                                                                                                                                                                                                     SLYFGRELETLPMCVLSAIIVIALKSMLWKLRDLKGIWKLSKIDCCIWMVAFFATVLVDV
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A;Gene: CESP:F14D12.5
A;Introns: 3/3; 53/2; 77/1; 159/3; 181/2; C;Superfamily: sulfate transport protein A;Status: preliminary; translated from A;Molecule type: DNA A;Residues: 1-650 <MIN> submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F14D12.
A;Reference number: Z18457
A;Accession: T16077 hypothetical protein F14D12.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep_1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000 C;Accession: T16077 A;Cross-references: C;Genetics: R; Minx, Matches 179; Query Match Best Local 9 25 EKKDRTYP-----VGEKLRNAFRC---SSAKIKAVVFGLLPVLSWLPKYKIKDYII 72 Similarity Conservative EMBL: U41021; 16.3%; 24.1%; 145; NID:g1086679; PID:g1086682; PIDN:AAA82335.1; Score 631; DB 2; Pred. No. 1.2e-40; 5; Mismatches 290 GB/EMBL/DDBJ 215/3; 270/3; Length 650; Indels 128; 321/1; 443/3; Gaps 479/2;

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EEYDQMYSFNREGNETWVKKKINN--YCTFLSKDGIRKIILRRVPVIDWIGSYQINNF-A 60

17;

503/3;

CESP:F1

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18;

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A;Cross-references: EMBL:U67954; PIDN:AAB52608.1; GSPDB:GN00028; CESP:F41D9.
A;Experimental source: strain Bristol N2; clone F41D9
C;Genetics:
                                                                                                                                                                                                                                hypothetical protein F41D9.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t C;Accession: T25751 R;Fulton, B.
   A; Map position:
A; Introns: 5/3;
C; Superfamily: s
                                                                                                               A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-758 <FUL>
                                                                                                                                                                                submitted to the EMBL Data Library, August 1996 A; Description: The sequence of C. elegans cosmi. A; Reference number: Z20081
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   Superfamily: sulfate
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                                                   CESP: F41D9.5
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74/1; 111/1; 165/2; 206/3; sulfate transport protein
                                                                                                                                                                                                                                                                                                                                                                                   -KMFFDCEKSM 643
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                                                                                                                                                                                                                                                                  15-Oct-1999 #text_change
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                  261/3;
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                  313/3;
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                  370/3;
                  466/3;
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                 502/2; 551/3;
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20

Query Match

15 . 28;

Score 588;

DВ 2;

Length

A;Gene: CESP:W04G3.6 A;Map position: X A;Introns: 46/1; 83/1; 135/3; 153/3; 190/3; 244/3;

272/2

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hypothetical protein W04G3.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T26165
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T26165
A; Experimental source: C; Genetics:
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                                   A; Cross-references:
                                                 A; Molecule type: DNA
A; Residues: 1-380 <WIL>
                                                                               A;Accession: T26165
A;Status: preliminary; translated from
                                                                                                                  A; Reference number: Z20163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPLYFANSEIFROKVIAKTVSLQELQQDFENAPPTDPNNNQTPANGTSVSYIT---FSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DMGEGLLMAIGFAVLTTIIRTQRPKWHFLSRDDDTENYKETKKRD-LERIQGNVCIFRMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKLR--YACSPSKCIHSLLSFLPIITWLPKYDWSHSFFGDLSGGLTMAVFSVPQGIALAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKLRNAFRCSSAKIKAVVFGLLPVLSWLPKYKIKDYIIPDLLGGLSGGSIQVPQGMAFAL
                                                                                                                                                                                                                                                                                                                                       STYGKIGVKVFLVNIHAQVYNDISHGGVFEDGSLECKHVFPSIHDAVLFAQ
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                                                                                                                                                                                                                                                                                                                                                                                                          SSSPAQSEPPASAE---APGEPSDMLASVPPFVTFHTLILDMSGVSFVDLMGIKALAKLS
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                                 EMBL: Z68014; PIDN: CAA92028.1;
                   clone
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                                                                                                                                    Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                             -TMSVWQCVKKWERC-------KSESFVTIEQMNSD
                   W04G3
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1; Mismatches 295;
                                                                                                                                     November
                                                                                    GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                            -LVIDCDGFPYVDYLGLSTLKSVY
                                   GSPDB:GN00028;
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Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Cansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A.; Lil, J.H.; Lil, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A.; M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A.; Reference and analysis of chromosome 1 of the plant Arabidopsis.
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C; Superfamily: sulfate transport protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE005172; NID:g2829902; PIDN:AAC00610.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-631 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A86141; A; Accession: B86365
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                                                                                                                                                                                                                                        TLFDDEFEKKDRTYPVGEKLRNAFRCSSAKIKAVVFGLLPVLSWLPKYKIKDYIIDDLLG 77
YLSESFIRGFMTAAGLQILISVLKYIFGLTIPSYTGPGSIVFTFIDICKNLPHTN-----
                                                MLRQ----
                                                                                                                            GLTIASLAIPQGISYAKLANLPPIVGLYSSFVPPLVYAVLGSSRDLAVGPVSIASLILGS 132
                                                                                                                                                        GLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLGGVHQMVPGTFAVISILVGN 137
                                                                                                                                                                                                                TFFPDDPLRQFRGQPNRTKL-----IRAAQY-IFPILQWCPEYSF-SLLKSDVVS 72
                                                                                    ICLQLAPESKFQVFNNATNESYVDTAAMEAERLHVSATLACLTAIIQMGLGFMQFGFVAI 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KVIAKKHNYEIDVRQEFFALGIVASTCSMFPCWPATTALARTLINDNAGTKTQV
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                                                                                                                                                                                                                                                                                                    14.2%; Score 549; DB 2; al Similarity 26.0%; pred. No. 2.5e-34; 175; Conservative 120.
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                                            SPVDDPVLFLQ-LAFSSTF--FAGLFQASLGILRLGFIID 175
                                                                                                                                                                                                                                                                                                    120; Mismatches 251; Indels 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 148;
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_cha
C;Accession: T48901
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                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: ATST1 C;Superfamily: sulfate transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-658 <SOH>
A; Cross-references: EMB!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Sohlberg, L.E.; Sussex, I.M.
Plant Physiol. 113, 1463, 1997
A;Title: Nucleotide sequence o.
A;Reference number: Z15626
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:D89631; A;Experimental source: Landsberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: T48901
A;Status: preliminary; translated
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Best Local
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                                                                                                                              VLSWLPKYKIKDYIIPDLLGGLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFL 117
                   GSSRDLAVGTVAVASLLTG---AMLSKE---
                                                           GGVHOMVPGTFAVISILVGNICLQLAPESKFQVFNNATNESYVDTAAMEAER-----LHV 172
                                                                                                     IFEWAPRYNLK-FFKSDLIAGITIASLAIPQGISYAKLANLPPILGLYSSFVPPLVYAVL 128
                                                                                                                                                                                       PQPQPFLKSLQYSVKETLFPDDPFRQ-----FKNQNASR-----KFVLGLKYFLP
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                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                            14.1%; Score 544.5; DB 2; ilarity 24.9%; Pred. No. 5.8e-34; Conservative 127; Mismatches 274;
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                      VDAEKDPKLYLHL
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parts

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A; Molecule type: DNA
A; Residues: 1-658 <ALC>
A; Cross-references: EMBL: AL049711; GSPDB: GN00061; ATSP: F4F15.10
A; Experimental source: cultivar Columbia; BAC clone F4F15
C; Genetics:
A; Gene: ATSP: F4F15.10
                                                                                                                                                                                                                                                                                                                                                                                                                                       sulfate transporter (ATST1) - Arabidopsis thaliana
N;Alternate names: protein F4F15.10
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 21-Jul-2000
C;Accession: T49069
R;Alcaraz, J.P.; Clabault, G.; Cottet, A.; Mache, R.; Mewes, H.W.; Rudd, S.; submitted to the Protein Sequence Database, April 2000
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A; Accession: T49069
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;Introns: 116/1; 185/2;
;Superfamily: sulfate to
                                                                                                                                 Query Match
Best Local Similarity
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58 VLSWLPKYKIKDYIIPDLLGGLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFL
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                                                             PRPRYVVDRAAYSL--TLF-DDEFEKKDRTYPVGEKLRNAFRCSSAKIKAVVFGL---LP
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                                     PQPQPFLKSLQYSVKETLFPDDPFRQ-----FKNQNASR-----KFVLGLKYFLP
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                                                                                                                 Conservative 127;
                                                                                                                                                                                                          transport protein
                                                                                                                                                                                                                              242/3; 264/3; 302/3;
                                                                                                                                 14.0%; Score 543.5; DB 2; 24.9%; Pred. No. 7e-34;
                                                                                                                 Mismatches
                                                                                                                                                                                                                              341/3; 384/1; 479/3; 543/2; 572/1;
                                                                                                                 274;
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hypothetical protein [imported] - Arabidopsis thaliana c;Specles: Arabidopsis thaliana (mouse-ear cress) C;Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 02-Sep-2000 C;Accession: T51161
                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
T51161
                                                                                          A;Map position: 3
A;Introns: 161/1; 230/2
C;Superfamily: sulfate
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                                                                                                                                                                    A; Cross-references:
                                                                                                                                                                                   A; Residues: 1-703 <C
                                                                                                                                                                                                                                             A; Accession: T51161
                                                                                                                                                                                                                                                            A; Title: Fine sequence analysis of 60~\rm{kb} around the Arabidopsis thaliana AtEml locus A; Reference number: 224835; MUID: 20108326
                                                                                                                                                                                                                                                                                                 R;Comella, P.; Wu, H.J.; Laudie, M.; Berger, C.; Cooke, Plant Mol. Biol. 41, 687-700, 1999
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                                                                                        230/2; 287/3; 309/3; 347/3; lfate transport protein
                                                                                                                                                                    EMBL: AF049236; PIDN: AAC14417.
14.0%; Score 543.5; DB 2; 24.9%; Pred. No. 7.7e-34; tive 127; Mismatches 274;
                                                                                                              386/3; 429/1; 524/3; 588/2;
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                                                                                                              617/1;
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Matches

180;

Conservative

Indels

141;

Gaps

23;

642/

Similarity

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R;Bradshaw, H.; Graves, T.; Blair, T. submitted to the EMBL Data Library, January 1998 A;Description: The sequence of C. elegans cosmid A;Reference number: Z21250 A;Accession: T32945
A; Introns: 15/2
                                            A; Cross-references: EMBL: AF043704; A; Experimental source: strain Brist C; Genetics:
                                                                                                                                                                                                          hypothetical protein W01B11.2 - Caenorhabditis elegans C;SpecLes: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #te:C;Accession: T32945
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                                                                                       A; Molecule type: DNA
A; Residues: 1-809 < BRA>
                                                                                                                    A; Status: preliminary; translated
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                                CESP:W01B11.2
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   15/2;
                                                                                                                                                                                                                                                                                                                                                            696
   38/3;
   114/1;
                                                          3704; PIDN:AAB97595.1; GSPDB:GN00019; Bristol N2; clone W01B11
   269/3;
                                                                                                                    from GB/EMBL/DDBJ
420/1; 497/1; 518/2;
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 648/1;
 684/1;
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Length
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C; Superfamily: sulfate

transport protein

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RESULT
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Best Local
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                15
                                                                VSVSDAVDQAELEQRHKTETVQTTAAP
                                                                                                    PSIHDAVLFAQANARDVTPGHNFQGAP 716
                                                                                                                                                      DMSGVSFVDLMGIKALAKLSSTYGKIGVKVFLVNIHAQVYNDISHGGVFEDGSLECKHVF
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                                                                                                                                    DCSTIIYVDLMGQGALKDVYNDYKTIGISVLFANTNEHVRQNFETSQFFEE--VPRGRMF
                                                                                                                                                                                                                                       TDPNNNQTPANGTSVSYITFSPDSSSPAQSEPPASAEAPGEPSDMLASVPPFVTFHTLIL
                                                                                                                                                                                                                                                                         IKIFRFDSPIYFGNSEMFVRKIHQACGLNPLIVRGELETENKKKDARKEKEEEDAEIPKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RISNVPPTSEPFQNVVFYMCFFKQMPDVDYASIIISVICVVLLLISTLVIDPWLCKKVPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLT-IPSYTGPGSIVFTFIDICKNLPHTNIASLIFALISGAFLVLVKELNARYMHK---I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDGDATGIAASVTLLVGLFQILFGLLNAGLLAVWLSDQLVQGLISGAAVHVLTSQLKSMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRIPITMWLPRYTWKSNFLVDFLGGLMVSVLSVPQSLAYGMLVGVPPSYGLITGIIGPII
                                                                                                                                                                                                     TEKE----PADQYERLTHI-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HFCVWRSCWMYSALAETGARVDCGCCDEGLVHSDFHLLRVEEIEFCGLCELRGGKPGVRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEAERLHVSATLACLTAIIQMGLGFMQFGFVAIYLSESFIRGFMTAAGLQILISVLKYIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YALFGTSKHSSPGAFAIVSLMVGTVV-----ESFGDVGSTNGTIDSNVDLLCCRENKPRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -CALSVTLAVDGA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 532.5; DB 2;
Pred. No. 6.6e-33;
B; Mismatches 274;
                                                                                                                                                                                                                                                                                                       ---IAKTVSLQELQQDFENAPP
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sulfate transporter AST12 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_ch. C;Accession: T48902

밁 Ş B 20 밁 Ş 밁 Ş 밁 Ş 밁 δÃ 밁 Ωy 밁 Š 밁 Š Вb QY 밁 δÃ 망 Ş B δÃ

A;Title: Identification of two A;Reference number: Z25001 A;Accession: T48902

Plant Physiol. 121, 686, R;Takahashi, H.;

Sasakura,

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Kimura,

Α.,

Watanabe,

Saito,

#text_change Α.,

21-Jul-2000

leaf-specific sulfate

transporters

in

Arabidopsis thal

A;Status: preliminary; A;Molecule type: DNA

translated

from

GB/EMBL/DDBJ

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A;Residues: 1-646 <TAK>
A;Cross-references: EMBL:AB012048; PIDN:BAA25175.1
A;Cross-references: ecotype Columbia
A;Experimental source: ecotype Columbia
C;Genetics:
A;Map position: 3
A;Introns: 116/1; 185/2; 242/3; 264/3; 302/3; 329/3; 372/1; 467/3; 531/2; 560/1; 585/3
C;Superfamily: sulfate transport protein
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                                                                                                                                                                                                  451
                                                                                                                                                                                                                                                               392 IVMAIAVMETLLELTPLEHYTPLVVLSAII-ISAMLGLIDYQAAIHLMKVDKFDELVCMS
                                                                                                                                                                                                                                                                                                      409
                                                                                                                                                                                                                                                                                                                                       332
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279 PLTSVILGSLLVYFTHAERHG-VQVGSDLIFTSPYMSTA-----VKTGLITGIIALAEG 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129
575 IKKVIDRRALKLVLSNPKGEVVKKLTRSKFIGD-HLGKEWMFLTVGEAV 622
                                                                                                                                                                                                                                   469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173
                                                                                                                                                                                                                                                                                                                                                                                                                                   293 VATAISGGCKMPKKYHMQIVGEIQRG----FPTPVSPVVSQWKDMIGTAFSLAIVSYVIN 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25
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                                                                                                                                                                                                                                                                                                                          GPGSIVFTFIDICKNLPHTNIASLIFALISGAFLVLVKELNARYMHKIRFPIPTEMIVVV 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGVHQMVPGTFAVISILVGNICLQLAPESKFQVFNNATNESYVDTAAMEAER-----LHV 172
                               LSSTYGKIGVKVFLVNIHAQVYNDISHGGVFEDGSLECKHVFPSIHDAV 696
                                                                                               TFSPDSSSPAQSEPPASAEAPGEPSDMLASVPPFVTFHTLILDMSGVSFVDLMGIKALAK 647
                                                                                                                                                                IKIITYCSPLYFANSEIFRQKVIAKTVSLQELQQDFENAPPTDPNNNQTPANG-TSVSYI 587
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                                                                -----ILDMSAVGNIDTSGISMMVE
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Search completed: April 26, 2002, 09:06:02 Job time: 208 sec

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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

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Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-136-7049-9
US-08-130-001-4
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Matches

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Conservative

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Indels

68;

Gaps

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1120; DB 1; No. 1.7e-101;	US-08-424-567-2 Sequence 2, Application US/08424567 Patent No. 5569755 GENERAL INFORMATION: APPLICANT: SCHWEINFEST, Clifford W. APPLICANT: SCHWEINFEST, Clifford W. TITLE OF INVENTION: Colon Mucosa Gene Having Down: TITLE OF INVENTION: Expression In Colon Adenomas & NUMBER OF SEQUENCES: B CORRESPONDENCE ADDRESS: ADDRESSE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington, D.C. COUNTRY: USA ZIP: 20007-5109 COMPUTER READABLE FORM: MEDIUM TYPE: TIDAPY disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIA PLICATION DATA: APPLICATION NUMBER: US/08/424,567 FILING DATE: DATE: CLASSIFICATION NUMBER: US/08/424,567 FILING DATE: O5-MAR-1993 ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 40399/181 NIHD TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5390 TELETAX: 904136 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHRACTERISTICS: LENGTH: 764 amino acids TYPE: amino acids TYPE: amino acids TYPE: molical acids TYPE: molical acids TYPE: protein	ALIGNMENTS	28 99 2.6 574 3 US-09-042-913-7 29 99 2.6 574 3 US-09-188-496-6 30 99 2.6 574 3 US-09-042-937-7 31 99 2.6 574 4 US-09-397-238A-4 32 96.5 2.5 401 3 US-08-492-459-8 33 96.5 2.5 401 3 US-08-492-459-2 36 96.5 2.5 401 3 US-08-492-459-2 37 96.5 2.5 401 3 US-08-492-459-2 38 96.5 2.5 401 3 US-08-492-459-2 39 96.5 2.5 401 3 US-08-423-752-8 39 96.5 2.5 401 4 US-08-716-873-2 40 96.5 2.5 401 4 US-08-716-873-2 41 96.5 2.5 401 4 US-08-716-873-2 42 96.5 2.5 401 4 US-08-716-873-4 43 96.5 2.5 401 4 US-08-716-873-4 44 96.5 2.5 401 4 US-08-716-873-4 45 96.5 2.5 401 4 US-08-716-873-4 46 96.5 2.5 401 4 US-08-716-873-4 47 96.5 2.5 401 4 US-08-716-873-4 48 96.5 2.5 401 4 US-08-716-873-4 49 96.5 2.5 401 4 US-08-716-873-4 40 96.5 2.5 401 4 US-08-716-873-4 41 96.5 2.5 401 4 US-08-716-873-4 42 96.5 2.5 401 4 US-08-716-873-4 43 96.5 2.5 401 4 US-08-716-873-4 44 96.5 2.5 401 4 US-08-716-873-4
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US-08-711-928-2

: Sequence 2, Application US/08711928

: Patent No. 5831015
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APPLICANT: SCHWEINFEST, Clifford W.
APPLICANT: PAPAS, Takis S.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Flop COMPATIBLE
COMPUTER: FLOP POS MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Colon Mucosa Gene Having Down-Regulated TITLE OF INVENTION: Expression In Colon Adenomas And Adenoc
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                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                               ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., CITY: Washington, D.C.
                                                                                                                                                          COUNTRY:
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TOPOLOGY: linear; MOLECULE TYPE: protein US-08-711-928-2
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Best Local :
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APPLICATION NUMBER: US 08/026
FILING DATE: 05-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 4039
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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LENGTH: 764 amino acids
TYPE: amino acid
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APPLICATION NUMBER: US.
FILING DATE: 11-SEP-19
CLASSIFICATION: 435
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YFANIGFFRRKLIDAVGFSPLRILRKRNKALRKIRKLQKQGLLQVTPKGFICTVDTIKDS
                                                    YFANSEIFROKVI------AKTVSLQELQQ-----
                                                                                                              GLGLAASVAFQLLTIVFRTQFPKCSTLANIGRTNIYKNKKDYYDMYEPEGVKIFRCPSPI
                                                                                                                                              PYGVAVGVAFSVĹVVVFQTQFRNGYALAQVMDTDIYVNPKTYNRAQDIQGIKIITYCSPL 538
                                                                                                                                                                                                                          VLAIGFLLAPLQKSVLAALALGNLKGMLMQFAEIGRLWRKDKYDCLIWIMTFIFTIVLGL
                                                                                                                                                                                                                                                                                  MLVLGIYLYPLPKSVLGALIAVNLKNSLKQLTDPYYLWRKSKLDCCIWVVSFLSSFFLSL 478
                                                                                                                                                                                                                                                                                                                                            YDYPLDGNQELIALGLGNIVCGVFRGFAGSTALSRSAVQESTGGKTQIAGLIGAIIVLIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           YGCDFKNRFKVAVVGDMNPGFQPPITPDVETFQNTVGDCFGIAMVAFAVAFSVASVYSLK 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCKMPKKYHMQIVGEIQRGFPTPVSPVVSQWKDMIGTAFSLAIVSYVINLAMGRTLANK 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTFIDICKNLPHTNIASLIFALISGAFLVLVKELNARYMHKIRFPIPTEMIVVVVATAIS
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34.0%; Pred. No. 1.7e-101;
htive 142; Mismatches 275;
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                                                                                                           Matches
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Best Local :
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                                                                                                                                                                                                                                                                            TELEFAX: (202)672-539
TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 40 TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                                                                                                                        Local
                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/184,937
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               KIKDYIIPDLLGGLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLGGVHQMVP 125
                                          QYIVARPVYSTNAFEENHKKTGRHHKTFLDHLKVCCSCSPQKAKRIVLSLFPIASWLPAY
                                                                         RYVVDRAAYSLTLEDDEFEKKDRTYPVG-EKLRNAFRCSSAKIKAVVFGLLPVLSWLPKY 65
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                                                                                                          1 Similarity
250; Conser
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28.9%;
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                                                                                                        Score 1120; DB 4;
Pred. No. 1.7e-101;
2; Mismatches 275;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                          APPLICANT: CAO, LIANG
APPLICANT: ROSEN, CRAIG
TITLE OF INVENTION: HUMAN AMINE TRANSPORTER
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/471,496
                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                 CITY:
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CLASSIFICATION:
                   FILING DATE:
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VKSSIFFLTIHDAVL 718
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1100 NEW YORK AVENUE,
                                                                                                                                                                                                        USA
                     06-JUN-1995
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; MOLECULE TYPE:
US-08-471-496-2
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Best Local :
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                                                                                                                      APPLICANT: CAO, LIANG A. APPLICANT: ROSEN, CRAIG A. TITLE OF INVENTION: HUMAN AMINE TRANSPORTER NUMBER OF SEQUENCES: 9
                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 470 amino acid
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REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
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                         COUNTRY:
                                                                              ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVENUE, SUITE 600
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01-MAR-1995
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                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                     Sequence 2, Application US/09139675A Patent No. 6117426
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Best Local
APPLICANT: Li, Yi
APPLICANT: Cao, Liang
APPLICANT: Rosen, Craig
APPLICANT: Rosen, Craig
TITLE OF INVENTION: Human Amine Transporter
FILE REFERENCE: 1488.0830003
CURRENT APPLICATION NUMBER: US/09/139,675A
CURRENT FILING DATE: 1998-08-25
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,840
FILING DATE: 29-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                      MIGTAFSLAIVSYVINLAMGRTLANKHGYDVDSNQEMIALGCSNFFGSFFKIHVICCALS
                                                                                                                                                                                                                                                                                                           VTLAVDGAG---GKSQVASLCVSLVVMITMLVLGIYLYPLPKSVLGALIAV
                                                                                                                                                                                                                                                                                                                                                QLGLAFLPASVSYLIGTNLFGVLANKMGRWLCSLIGMLVVGTS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MHKIR----FPIPTEMIVVVVATAISGGCKMPKKYHMQIVGETQRGFPTPVSPVVSQWKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGTALGGLALGLLVGAPFGSVMYEFVG--KSAPFLILAFL--ALLDGALQLCILQPSKVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QRLLKEGRASRQLVLVVVFVALLLDNMLFTVVVPIVPTFLYDMEFKE-VISSLHLGHAGS 68
                                                                                                                                                                                                                                                                        VPLAHKNFGLIGPNAGLGLXIGMVESSMMPIMGHLVDPRHTSVYGSVHAI
                                                                                                                                                                                                                                                                                                                                                                                                                         PESAKGTPLFMLLKDPYILVAAGSI---C----FANMGVAILEPTLPIWMMQTMCSPKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --KYIFGLTIPSYTGP--GSIVFTFIDICKNLPHTNIASLIFALISGAFLVLVKELNARY 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -MQFGFVAIYLS-------ESFIRGFMTAAGLQILISVL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APESKFQVFNNATNESYVDTAAMEAERLHVSATLACLTAIIQM------GLGF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S---PHALA-----SPAFSTIF-SFFNNNTV----AVEESVPSGIAWMNDTASTI---- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PMFAGFVIMFLSTVMFAFSGTYTLLFVARTLQGIGSSFSSVAGLGMLASVYTDDHERGRA
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Pred. No. 0.0015;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184;
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Indels 111; Length 470;

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: LOCATION: (402)
: OTHER INFORMATION: May be
US-09-139-675-2
                                                                                                                                                                                                                                                                                                                                                    US-09-110-116-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 2
                                          SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3 LENGTH: 886
                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09110116 Patent No. 6013479
                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                        APPLICANT: Xu, Hong
APPLICANT: Cohan, Victoria L.
APPLICANT: Stuart, Susan G.
TITLE OF INVENTION: HUMAN EMR1-LIKE G
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: WO PCT/US95/02645
EARLIER FILING DATE: 1995-03-01
EARLIER FILING TON NUMBER: US 08/471,496
EARLIER FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
                                                                                                    FILE REFERENCE: PF-0550 US
CURRENT APPLICATION NUMBER: US/09/110,116
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 4
TYPE: PRT
ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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les 105; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTLAVDGAG--GKSQVASLCVSLVVMITMLVLGIYLYPLPKSVLGALIAV 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIGTAFSLAIVSYVINLAMGRTLANKHGYDVDSNQEMIALGCSNFFGSFFKIHVICCALS 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -MQFGFVAIYLS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QRLLKEGRASRQLVLVVVFVALLLDNMLFTVVVPIVPTFLYDMEFKE-VISSLHLGHAGS 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKLRNAFRCSSAKIKAVVFGLL------PVL-SWLPKYKIKDYIIPDLLGGLSGG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLGLAFLPASVSYLIGTNLFGVLANKMGRWLCSLIGMLVVGTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MHKIR----FPIPTEMIVVVVATAISGGCKMPKKYHMQIVGEIQRGFPTPVSPVVSQWKD 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --KYIFGLTIPSYTGP--GSIVFTFIDICKNLPHTNIASLIFALISGAFLVLVKELNARY 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APESKFQVFNNATNESYVDTAAMEAERLHVSATLACLTAIIQM------GLGF-- 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S---PHALA-----SPAFSTIF-SFFNNNTV----AVEESVPSGIAWMNDTASTI---- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLGGVHQMVPGTFAVISILVGNICLQL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGTALGGLALGLLVGAPFGSVMYEFVG--KSAPFLILAFL--ALLDGALQLCILQPSKVS 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PMFAGFVIMFLSTVMFAFSGTYTLLFVARTLQGIGSSFSSVAGLGMLASVYTDDHERGRA 228
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Pred. No. 0.0015;
0; Mismatches 184;
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; OTHER INFORMATION: 784994, GenBank
US-09-110-116-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-843-417-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/08843417 Patent No. 6184349
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Best Local
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TELEFAX: (415)-324-063
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Delgado, Stephen G
APPLICANT: Fish, Linda M
APPLICANT: Sangameswaran, Lakshmi
APPLICANT: Rabert, Douglas K
                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                                                      REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 28
                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                         APPLICATION NUMBER: US/08/8 FILING DATE: April 15, 1997
                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                       CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGELTMDFSLYIISHVGIIISLVCLVLAIATFLLCRSIRNHNTYLHLHLCVCLLLAKTLF 652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GRTLANKHGYDVDSNQEMIALGC----SNFF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
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63; Conser
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                                                                                                                                                                                                                                                                                                                                                          CA
                                                                                                                                                                                                                                                                                                                                                                                             525 University Ave
                                                                                                                                                                                                                                                                                                                                       U.S.A.
                                  (415)-324-0638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rabert, Douglas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Herman, Ronald C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SPVVSQWK-DMIG---TAFSLAIV----SYVI-----NLAM--- 351
                                                     (415)-324-7041
                                                                                                                                                                                                                                                                                                                                                                                                           Heller Ehrman White & McAuliffe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - VVNYFSSRNIKMLHICAFGYGLPMLVVVISASVQPQGYG----
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                                                                                                                                                                                               US/08/843,417
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                                                                                        28340-P1
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Pred. No. 0.32;
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                                                                                                                                                                                                                                  Version
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                                                                                                                                                                                                                                  #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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; TYPB: amino acid
; STRANDEDNESS: unkn
; TOPOLOGY: unknown
; MOLECULE TYPE: pepti
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-843-417-10
                                                                                                                                                                                                                                                                                                                                 RESULT 9
US-08-677-049-9
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                                                                                                                                                                                                                                                                   Sequence 9, Application US/08677049 Patent No. 5858707 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.7%; Score 103.5; Best Local Similarity 19.4%; Pred. No. 1.5; Matches 112; Conservative 93; Mismatches
                                                                                                                                       APPLICANT: Guimaraes, M. Jorge
APPLICANT: Bazan, J. Fernando
APPLICANT: McClanahan, Terrill K.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: PURIFIED MAMMALIAN NUCLEOBASE PERMEASES;
TITLE OF INVENTION: NUCLEIC ACIDS; ANTIBODIES
                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1013 GGEDAQSFQQEVIPKGQQEQLQQVERCGDHLTP-----RSPGTGTSSEDLAPSLGETWK 1066
STATE: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      539 YFANSEIFRQKVIAK--TVSLQELQQDFENAPPTDPNNNQTPANGTSVSYITFSPDSSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      385 HVICCALSVTLAVDGAGGKSQVASLCVSLVVMITMLVLGIYLYPLPKSVLGALIAVNLKN 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               636 TSLSOKYLIWDCCPMWVKLKTILFGLVTDPFAELTI-----TLCIVVNTIFMAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 TAIIQ-----MGLGFMQFGFVAIYLSESFIRGFMTAAGLQILISVLKYIF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 QMVPGTFAVISILVGNICLQLAPESKFQVFNNATNESYVDTAAMEAERLHVSATLA--CL 179
                                                            STREET:
                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSSSKAENHIAANTARGSSGGLQAPRGPRDEHSDFTANPTVWVSVPIAEGESDLDDLEDD 1012
                                                                                                                                                                                                                                                                                                                                                                                                                DESVPQAPAEGVDDTSSSEGSTVDCLDPEEILRKIP 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SLKQLTDPYYLWRKSKLDCCTWVVSF-----LSSFF-LSLPYGVAVGVAFSVLVVV 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQSEPPASAEAPG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGNLTITLATIVEVEAL-VGKQLL---GENYRNNRKNISAPHEDWPRWHMHDFFHSFLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----AFSLAIVSYVINLAMGRTLANKHGYDVDSNQEMIAL-----GCSNFFGSFFKI 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KWNIFDCIIVTVSLLELGVAKKGSLSVLRSFRLLRVFKLAKSWPT-LNTLIKIIGNSVGA 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RFPIPTEMIVVV----VATAISGGCKMPKKYHMQIVGEIQRGFPTPVSPVVSQWKDMIGT 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --GL--TIPSYTGPGSIVFTFIDICKNLPHTNIASLIFALISGAFLVLVKELNARYMHKI 280
                                        T: 901 California Avenue
Palo Alto
                     California
  USA
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                                                                                 DNAX Research Institute
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NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----EPSDMLASVP 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93; Mismatches 244; Indels 127;
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LOCATION: 359..386
COTHER INFORMATION: 4"
US-08-677-049-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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MEDIUM TYPE: Floppy
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LOCATION: 323..357
OTHER INFORMATION: ,
OTHER INFORMATION: ,
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LOCATION: 115..144
OTHER INFORMATION: OTHER INFORMATION:
   471
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                                                                                                                                                                                               314
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                                                                                                                                                                                                                                                                                            121 FPPVVTGSVVTIIGITLMPVAMN----NMAGGEGSADFGDLSNLALAFTVLSIIVLLYRF 176
                                                                                                                                                                                                                                                                                                                                                                               172 VSATLACLTAIIQMGLGFMQFGFVAIYLSESFIRGFMTAAGLQILISVLKYIFGLTIPSY 231
                                                                                               270 YRAEGLAVLLGGIFN-----AFPYT-AFSQNVGLVQLTGIKKNAVIVVTGVILMAFGLF
                                                                                                                                                                                                                                                                                                                            232 TGP---GSIV----FTFIDICKNLPHTNIA------SLIFALISGAFL----
                                                                                                                                                                                                                                                                                                                                                            74 LGCTFTAVSPMIAIG---SEYGVSTVY------GSIIASG--ILVILISFFFGKLV-SF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/000,788 FILING DATE: 03-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/677,049 FILING DATE: 03-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 2.7%;
Local Similarity 19.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
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                                                                                                                                                                                  EIQRGFPT-PVSPVVSQWKDMIGTAFSLAIVSYV----INLAMGRTLANKHGYDVDSNQE 368
                                                                                                                                                                                                                              TKGFIKSVSILIGILIGTFIAYFMGKVQFDNVSDAAVV--
                                                                                                                               MIALGCSNFFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMITMLVLGIY-LY
                                                                                                                                                               PFYFGAPSFHAAPII-----TMSIVAIVSLVESTGVYFALG-DLTNRRLTEIDLSKG 269
                                 PKIAAFTTIIPSAVLGGAMVAMFGMVIAYGIKMLSRIDFAKQENLLIVACSVGLGLGVTV 382
                                                            P-----LPKSVLG----ALTAVNLKNSLKQLTDPYYLWRKSKL--DCCIWV---VSF
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 YGVAVGVAFSVLVVVFQTQFRNGYALAQVMD
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Pred. No. 0.14;
6; Mismatches 132;
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US-08-861-464-4
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Matches
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                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 781-861-9540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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APPLICATION NUMBER: |
FILING DATE: 15-AUG-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/396,001
FILING DATE: 28-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Guarente, Leonard P.
APPLICANT: AUSTRIACO Jr., Nicanor
APPLICANT: Kennedy, Brian
TITLE OF INVENTION: Genes Determin
                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 16-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
 247
                                                                                                140
                                                                                                                                                                                                                                                                                                                                         TYPE: am TOPOLOGY:
                                 199
                                                                193
                                                                                                                             141 QLAPESKFQVF---NNATNESYVDTAAMEAERLHVSATLACLTAIIQMGLGFM-----QF
                                                                                                                                                              87
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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NLPHTNIASLIFALISGAFLVLVKELNARYMHKIRFPIPTEMIVVVVATAISGGCKMPKK 306
                                                                                            SVTPAASLRNFSNSNNAASKCGVDNSSFGLSS-STSSSMVEISALPLRDLDYIKLATDQF
                                                                                                                                                             ASMANPPAI------LPLINEFDLEMDGPRRKSSHDFTVVAPSNSGVNTSSLIMETPSS 139
                                                                                                                                                                                         ALLANLPAVNGLYSSFFPLLTYFFL--GGVHQMVPGTFAVI------SILVGNICL 140
                                                              G--FVAIYL---SES-FIRGEMTAAGLQILISVLKYIFGLTIPSYTGPGSIVFTFIDICK
                                GCRFLQKKLETPSESNMVRDLMYEQIKPFFLDLILDPFG----
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                                                                                                                                                                                                                                         Score 103; DB Pred. No. 0.41;
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                                -----NYLVQKLCD
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APPLICANT:
APPLICANT:
                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: FILING DATE: 28-FEE CLASSIFICATION: 435
                                                                                                                                                               COUNTRY:
                                                                                                                                                                              STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DS--NQEMIALGCSNFFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMITMLV 421
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                                                                                                                                                               USA
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Cole, Francesca
                                                                                                                                                                                                                                                                                                                                                            Austriaco Jr., Nicanor
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               28-FEB-1995
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                                                                                                                                                                                                                                                                              Yeast
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                              US/08/396,001
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                                                                 Version
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; TOPOLOGY: 11; MOLECULE TYPE: US-08-396-001-4

linear

protein

TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 834 mmino acids
TYPE: amino acid

TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540

ATTORNEY/AGENT INFORMATION:

Matches 140;

87

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Query Match 2.7%; Score 103; DB Best Local Similarity 17.6%; Pred. No. 0.41;
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REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-6408A2
                                                                                                                                            MNFNQNAYPSMGAPSFNSQTNPPLVS-HNSLQNFDNRQFANLMAHPNSAAPIHSFSSSNI
                                                                                            KVFLVNIHAQVYNDISHGGVF--EDGSLECKHVFPSIHDAVLFAQANARDVTPG-----
                                                  ----TNVNPNVSRGFKQPGFMMNETDKINANHFSP-----YSNANSQNFNESFVPRMQ 779
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TITLE OF INVENTION: GENES DETERMINING CELLULAR SENESCENCE IN
TITLE OF INVENTION: YEAST
FILE REFERENCE: 0050.1491-003
CURRENT APPLICATION NUMBER: US/09/323,433A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: US 08/396,001
PRIOR APPLICATION NUMBER: US 08/396,001
PRIOR FILING DATE: 1995-02-28
PRIOR FILING DATE: 1995-02-28
PRIOR APPLICATION NUMBER: PCT/US94/09351
PRIOR APPLICATION NUMBER: US 08/107,408
PRIOR FILING DATE: 1993-08-16
NUMBER OF SEQ ID NOS: 48
COPTWARE: PASTISEO FOR WINDOWS Version 3.0
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; LENGTH: 834
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-323-433A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
US-09-323-433A-4
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GN-YALQTLLDVKNYSPLLAYNKNSNAIGQNSSSTLNYGNFCNDFSLKIGNLIVLTKELL
                                                                                            EKFIKKLFRITTGFIVNNNGGASQRTAVASDDVINASMNILLTTIDIFTVNLNVLIRDNF
                                                                                                                                              SFFLSLPYGVAVGV---
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                                                                                                                                                                                                                                           ---LGIYLYPLPKSV-----LGALIAVNLKNSLKQLTDPYYLWRKSKLDCCIWVVSFLS 472
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Cole, Francesca
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GENERAL INFORMATION:
                                      [NFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: E
FILING DATE: 11-JUN-1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/806,178
FILING DATE: 13-DEC-1991
PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                FILING DATE: 14-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/132,9
FILING DATE: 07-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/084,729
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APPLICANT: YOSHIMOTO, TAKAYUKI
TITLE OF INVENTION: Human Retrovirus Receptor and
NUMBER OF SEQUENCES: 31
                 SEQUENCE CHARACTERISTICS:
                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
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                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 07/899,075 FILING DATE: 11-JUN-1992
                                                                         TELEFAX:
                                                                                                                             REGISTRATION NUMBER: 18, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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LENGTH:
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                                                        66441 PENNIE
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                                                                         (212) 869-8864
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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14-DEC-1990
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11-JUN-1993
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Avenue of the Americas
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; TOPOLOGY: lit
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US-08-132-990A-4
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Best Local S
Matches 96
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                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MERUELO, DANIEL
APPLICANT: YOSHIMOTO, TAKAYUI
TITLE OF INVENTION: Therefor
NAME: Livnat, Shmuel 3,949
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: MEI
TELECOMMUNICATION INFORMATION:
                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Livnat, Shmuel
                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                 STREET: 419 Sever CITY: Washington
                                                                                                                                                                                                                                                                               COUNTRY: U
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 NLPAVNGLYSSFFPLLTYFFLGGV-----HQMVPGTFAVISILV------GNI 138
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                                                                                                                      FILING DATE:
                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IAVNLKNSLKQLTDPYYLWRKSKLDCCIWV---VSFLSSFFLSLPYGV 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVYQMARTTEELDRVDQNELVSASESQTGFLPVAEKFSLKSILSPKNVEPSKFSGLIVNI
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                                                                                                                                        PCT/US92/09382
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Best Local S
Matches 96
                                                                                                                                                                                                          APPLICANT: Burnham, Martin
APPLICANT: Lonetto, Michael
APPLICANT: Warren, Patrick
TITLE OF INVENTION: NOVEL TETRACYCLINE RESISTANCE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08898976 Patent No. 5891670
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 202 628-5197 INFORMATION FOR SEQ ID NO:
              ZIP: 08543

COMPUTER READABLE FORM:
MEDIUM TYPP: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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LENGTH: 622 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       385 HV-ICCALSVTLAVDGAGGKSQVASLCVSLV-----VMITMLVLGIYLYPLPKSVLGAL 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       432 LVYQMARTTEELDRVDQNELVSASESQTGFLPVAEKFSLKSILSPKNVEPSKFSGLIVNI
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TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
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Local Similarity 20.5%; Pred. No. 0.4;
nes 96; Conservative 60; Mismatches 206; Indels 1
APPLICATION NUMBER:
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US/08/898,976
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Search completed: Job time: 203 sec

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 PLLTYFFLGGVHQMVPGTFAVISILVGNICLQLAPESKFQVFNNATNESYVDTAAMEAER 169
                                                                                 351
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                                       389 CALSVTLAVDGA------GGKSQVASLCVSLVVMITMLVLGIYLY
                                                                                                                                                                  291 IMEQIYHLQLDTTSLLLVPGYIVAVIVGALSGKIGEYLNSKQAIITAIILIALSLILPAF
                                                                                                                                                                                                            302 KMPKKYHMQI-----
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VAVSVGIAIAAALIDEKALNEPGNDALSSHEGIILIILGLMSIVGLVLE
                                                                                 AVGNHISIFVISMIFFAGSFALMYAPLLNEAIKTIDLNMTGVAIGFYNL-----IIN 402
                                                                                                                        SLA--IVSYVINL-----AMGRTLANKHGYDVDSNQEMIALGCSNFFGSFFKIHVIC 388
                                                                                                                                                                                                                                                    NWLYMIGALIAIIVFALYIKNAQRPLVNKSFFQNKRYASFLFIVFVMYAIQLGYIFTFPF
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Maximum DB seq length: 200000000
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                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /SIDSB/gcgdata,
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Copyright (c) 1993 - 2000 Compugen Ltd
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No.	Score	Match Length DB	ength		Ħ	Description
-	1259.5	32.6	758	21	AAY71067	Human membrane tra
2	1116	28.8	764	15	AAR60568	Down-regulated in
ω	974.5	25.2	739	20	AAY08929	Rat DTDST protein.
4	972	25.1	739	20	AAY08928	Human DTDST protei
ۍ	735.5	19.0	506	22	AAM15272	Peptide #1706 enco
6	735.5	19.0	506	22	AAM27737	Peptide #1774 enco
7	735.5	19.0	506	22	AAM03017	Peptide #1699 enco
8	601.5	15.5	143	22	AAM42394	Human polypeptide
9	576	14.9	593	21	AAY44945	Wheat sulphate per
10	566	14.6	680	21	AAY44943	Soybean sulphate p
11	566	14.6	688	21	AAY44935	Corn sulphate perm

45	44	43	42	41	40	39	38	37	36	ω 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
151.5	16	163	163	170	•	9.	179.5	191	201	220.5	225	237.5	240	253	253	255	288	332.5	355.5	355.5	385.5	403.5	425	425	437	452.5	498	537	538.5	543.5	543.5	543.5	549
3.9	4.2	4.2										٠							9.2					11.0			12.9		•	4		14.0	14.2
226	416	55	55	582	312	485	485	411	390	311	466	128	76	537	537	483	457	446	510	510	499	606	579	565	746	842	579	656	621	703	658	658	631
21	20	22	22	21	21	22	22	22	19	21	21	21	21	22	22	22	21	21	21	21	21	22	22	22	21	21	21	21	21	21	21	21	21
AAY44938	AAY37263	AAM33220	AAM19798	AAB07557	AAB42187	AAB76816	AAG91372	AAG82493	AAW98528	AAY44937	AAY95728	AAB40320	AAG03678	AAB76818	AAG90717	AAG83019	AAG32202	AAG29249	AAG32201 ·	AAG31622	AAG29248	AAE04904	AAG90917	AAB76817	AAY44358	AAY44359	AAY44936	AAY44944	AAY44942	AAG31620	AAG32200	_	AAG29247
Artichoke sulphate	Chlamydia trachoma	Peptide #7257 enco	#6232 e	Protein encoded by	Human ORFX ORF1951	Corynebacterium gl	C glutamicum prote	S. epidermidis ope	H. pylori GHPO 141	Corn sulphate perm	Cosmid cHRIM5 enco	Human ORFX ORF84 p	Human secreted pro	Corynebacterium gl	C glutamicum prote	S. epidermidis ope	Arabidopsis thalia				Arabidopsis thalia	Human transporter	C glutamicum prote	Corynebacterium gl		P. chrysogenum sut	Corn sulphate perm	Wheat sulphate per	Soybean sulphate p	is	Arabidopsis thalia	18	Arabidopsis thalia

ALIGNMENTS

RESULT AAY71067 ID AAY7 AAY71067 standard; Protein; Human membrane transport protein, MTRP-12. 29-AUG-2000 AAY71067; _ (first entry) 758

Human; membrane transport protein; MTRP-12; antiinflammatory; cytostatic; antithyroid; immunosuppressive; thyromimetic; antiidabetic; noctropic; antidiarrheic; neuroprotective; antidepressant; neuroleptic; artigout; antidelminthic; protozoacide; antibacterial; neuroleptic; antigout; diagnosis; prevention; treatment; membrane transport disorder; epilepsy; Menkes disease; diabetes; Parkinson's disease; neurological disorder; Alzhelmer's disease; depression; schizophrenia; immune disorder; allergy; inflammatory disorder; ALDS; Addison's disease; atherosclerosis; gout; Graves disease; Hashimoto's thyroiditis; microbial infection; cancer; cell proliferative disorder

Homo sapiens

Key	Locatio	Location/Qualifiers	
Modified-site	138		
	/note=	/note= "Phosphorylation site"	site"
Modified-site	174		
	/note=	<pre>/note= "Phosphorylation site"</pre>	site"
Modified-site	251		
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Modified-site	376		
	/note=	/note= "Phosphorylation site"	site"
Modified-site	574		
	/note=	/note= "Phosphorylation site"	site"

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The present sequence is a membrane transport protein,

MTRP-12 from Incyte clone 1733477 isolated from human BRSTTUTO8 cDNA

CC library. MTRP-12 shows homology to mouse transporter (GI 5359730)

CC and human transporter (GI 291964), and is expressed in nervous,

gastrointestinal and reproductive tissues.

CT the present sequence is useful in diagnosis, prevention and treatment

CC of disorders related with increased or decreased expression of MTRP

CC such as familial goitre, Menkes disease, diabetes, Parkinson's disease,

CC neurological disorders such as Alzheimer's disease, depression, epilepsy,

CC schizophrenia, immune/inflammatory disorders such as AlDS, Addison's

CC disease, allergies, atherosclerosis, Graves disease, gout, Hashimoto's

CC thyroiditis, viral, bacterial, fungal, parasitic, protozoal or

Fragments of MTRP polynucleotides are useful as targets in microarrays.

MTRP DNA is also useful for generating hybridisation probes useful in
                                                                                                                                                                                                                                                                                                                                                                04-NOV-1998;
24-NOV-1998;
22-DEC-1998;
26-FEB-1999;
                                                                                                                                                                                            Claim 1; Page 105-106;
                                                                                                                                                                                                                          Novel human membrane transport proteins useful for diagnosis, prevention and treatment of membrane transport disorders, immune/inflammatory disorders and cell proliferative disorder
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AAR60568 standard; Protein; 764 A

AAR60568;

01-APR-1995 (first entry)

Down-regulated in adenoma DRA tumor suppressor

down-regulated in adenoma; t
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transporter expression containing a DNA sequence encoding a mammalian sulfate transporter (expression product of the DTDST gene) and containing no DNA sequence of 5' translation region of the mammalian sulfate transporter gene. The invention also describes; (A) a method for screening a human bone/cartilage disease treating agent including the steps: (1) transforming an animal cell with the above vector, (2) culturing the animal cell in the presence of a sample and (3) detecting the increase in the sulfate ion intake to the cell; (B) a drug preparation for the treatment of human bone/cartilage disease containing

for

containing

This invention describes the construction of a novel vector for sulfate

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Best Local S
Matches 219
DTDST; human. expression vector; bone disease; cartilage disease; drug preparation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the above vector as the active component. The sulfate transporter gene-containing vector is high in expression efficiency. This sequence represents the rat DTDST protein used in the method of the invention.
                                                        Human DTDST protein
                                                                                       19-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                               VGEKLRNAFRCSSAKIKAVVFGLLPVLSWLPKYKIKDYIIPDLLGGLSGGSIQVPQGMAF 92
                                                                                                                                                                                                                                                                    -lelhtvvidcsaiqfldtagihtlkevrrdyeaigiqvllaqcnpsvrdslakgey---
                                                                                                                                                                                                                                                                                                 FVTFHTLILDMSGVSFVDLMGIKALAKLSSTYGKIGVKVFLVNIHAQVYNDISHGGVFED
                                                                                                                                                                                                                                                                                                                                                       QQDFENAPPTDPNNNQTPANGTSVSYITFSPDSSSPAQSEPPASAEAPGEPSDMLASVPP
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                                                                                                                                             standard;
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               sulphate transporter; screening;
treatment; cell sulphate ion intake;
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Matches 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes the construction of a novel vector for sulfate transporter expression containing a DNA sequence encoding a mammalian sulfate transporter (expression product of the DTDST gene) and containing no DNA sequence of 5' translation region of the mammalian sulfate transporter gene. The invention also describes; (A) a method for screening a human bone/cartilage disease treating agent including the steps: (1) transforming an animal cell with the above vector, (2) culturing the animal cell in the presence of a sample and (3) detecting the increase in the sulfate ion intake to the cell; (B) a drug preparation for the treatment of human bone/cartilage disease containing the above vector as the active component. The sulfate transporter gene-containing vector is high in expression efficiency. This sequence represents the human DTDST protein used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                   KSQVASLCVSLVVMITMLVLGIYLYPLPKSVLGALIAVNLKNSLKQLTDPYYLWRKSKLD
                                                                 TEMIVVVVATAISGGCKMPKKYHMQIVGEIQRGFPTPVSPVVSQWK---DMIGTAFSLAI
                                                                                                                                                                                                                                                                                                                                                                                    HQMVPGTFAVISILVGNIC---LQ------LAPESKFQVFNNATNESYVDTAAM 165
                                                                                                                                                                                                                                                                                                                                                                                                                  wlpkydlkknilgdvmsglivgillvpqsiaysllagqepvyglytsffasiiyfllgts
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WLPKYKIKDYIIPDLLGGLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLGGV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpyhrilierq-----eksdtnfkefvikklqkncqcspakaknmilgflpvlq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QPRPRYVVDRAAYSLTLFDDEFEKKDRTYP--VGEKLRNAFRCSSAKIKAVVFGLLPVLS
:| | :::| || || ::: | || || ||
htqlsgvvtalvlllvllviaplfyslqksvlgvitivnlrgalrkfrdlpkmwsisrmd
                                                                                                      VSYVINLAMGRTLANKHGYDVDSNQEMIALGCSNFFGSFFKIHVICCALSVTLAVDGAGG
                                                                                                                                       ielvvvvaatlashfgklhenynssiaghiptgf---mppkvpewnlipsvavdaiaisi
                                                                                                                                                                                                                                            LTIPSYTGPGSIVFTFIDICKNLPHTNIASLIFALISGAFLVLVKELNARYMHKIRFPIP
                                                                                                                                                                                                                                                                              ---aimvgstvtflagvyqvamgffqvgfvsvylsdallsgfvtgasftiltsqakyllg
                                                                                                                                                                                                                                                                                                               EAERLHVSATLACLTAIIQMGLGFMQFGFVAIYLSESFIRGFMTAAGLQILISVLKYIFG
                                                                                                                                                                                                                                                                                                                                               rhisvgifgvlclmigetvdrelqkagydnahsapslgmvsngstllnhtsdricdkscy
                                                                                                                                                                                                          lnlprtngvgslittwihvfrnihktnlcdlitsllcllvllptkelnehfksklkapip
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No. 3e-89;
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                    The present invention relates to human single exon nucleic acid probes (SEMP: see AAI10068-AAI28459). The present sequence is a peptide encode by one such probe. The SEMPs are derived from human HeLa cells. The SEM can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefor useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM15272 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probe; human; microarray;
                                   specification, but was obtained in
                                                                                                                                                                          Claim
                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                       WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM15272;
                        at ftp.wipo.int/pub/published_pct_sequences
                                                Note: The sequence data for this patent did not
                                                                                                                                                                                                                                                                                     (MOLE-)
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-02346359.
2000US-0024263.
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Best Local S
Matches 164
Probe; human; breast disease; breast cancer; develo inflammatory disease; proliferative breast disease;
                           Peptide #1699 encoded by probe for measuring breast gene expression
                                                   09-OCT-2001
                                                                       AAM03017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                          AAM03017 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                        enynssiaghiptgf---mppkvpewnlipsvavdaiaisilgfaitvslsemfakkhgy
                                                                                                                                                                VNIHAQVYNDISHGGVFEDGSLECKH----VFPSIHDAVLFAQAN 702
                                                                                                                                                                                                                                                                 VAVGVAFSVLVVVFQTQFRNGYALAQVMDTDIYVNPKTYNRAQDIQGIKIITYCSPLYFA
                                                                                                                                                                                                                                                                                                                                                                                                    KKYHMQIVGEIQRGFPTPVSPVVSQWK---DMIGTAFSLAIVSYVINLAMGRTLANKHGY
                                                                                                                                                                                                       PASAEAPGEPSDMLASVPPFVTFHTLILDMSGVSFVDLMGIKALAKLSSTYGKIGVKVFL
                                                                                                                                                                                                                                               NSEIFROKVIAKTVSLQELQQDFENAPPTDPNNNQTPANGTSVSYITFSPDSSSPAQSEP
                                                                                                                                                                                                                                                                                                          iaplfyslqksvlgvitivnlrgalrkfrdlpkmwsisrmdtviwfvtmlssallsteig
                                                                                                                                                                                                                                                                                                                             LGIYLYPLPKSVLGALIAVNLKNSLKQLTDPYYLWRKSKLDCCIWVVSFLSSFFLSLPYG
                                                                                                                                                                                                                                                                                                                                                                                                                              frnihktnlcdlitsllcllvilptkelnehfksklkapipielvvvvaatlashfgklh
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zing gene expression in human placenta .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.0%; Score 735.5; DB 2
31.2%; Pred. No. 1.6e-65;
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         development
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 non-carcinoma
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          disorder;
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Best Local S
Matches 164
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21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in a
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                              482
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          298
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         llvgvcfsifcvilrtqkpkssllglveesevfesvsayknlqtkpgikifrfvaplyyi
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The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast cancer, disorders prodifferative breast disease and non-carcinoma tumours.
                                                                                                                                                                                                         Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l single exon nucleic
human breast -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27; SEQ ID No 11757; 322pp;
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632368.
2000US-0632368.
2000US-0234687.
2000US-02346359.
2000US-0236359.
                           19.0%;
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0%; Score 735.5; DB 22
2%; Pred. No. 1.6e-65;
105; Mismatches 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probe used
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                                                         DB 22;
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     Indels
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                                                         506;
     45;
     Gaps
     9
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185 MGLGFMQFGFVAIYLSESFIRGFMTAAGLQILISVLKYIFGLTIPSYTGPGSIVFTFIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAVGVAFSVLVVVFQTQFRNGYALAQVMDTDIYVNPKTYNRAQDIQGIKIITYCSPLYFA
                                                                                                                                                                                                                                                                               enynssiaghiptgf---mppkvpewnlipsvavdaiaisiigfaitvslsemfakkhgy 177
                                                                                                                                                                                                               DVDSNQEMIALGCSNFFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMITMLV
                                                      iaplfyslqksvlgvitivnlrgalrkfrdlpkmwsisrmdtviwfvtmlssallsteig
                                                                                      LGIYLYPLPKSVLGALIAVNLKNSLKQLTDPYYLWRKSKLDCCIWVVSFLSSFFLSLPYG
                                                                                                                                                                 tvkanqemyaigfcniipsffhcfttsaalaktlvkestgchtqlsgvvtalvlllvllv
                                                                                                                                                                                                                                                                                                                                        KKYHMQIVGEIQRGFPTPVSPVVSQWK---DMIGTAFSLAIVSYVINLAMGRTLANKHGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   CKNLPHTNIASLIFALISGAFLVLVKELNARYMHKIRFPIPTEMIVVVVATAISGGCKMP
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RESULT
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04-FEB-2000;

19-MAY-2000;

17-JUL-2000;

14-JUL-2000;

16-SEP-2000;

06-SEP-2000;

06-SEP-2000;

08-SEP-2000;

25-SEP-2000;

25-SEP-2000;

13-OCT-2000;

108-NOV-2000;

108-NOV-2000;

108-NOV-2000;

108-NOV-2000;

117-NOV-2000;

117-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human polypeptide SEQ ID NO 127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JAN-2001; 2001WO-US01346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurological disease; infection; nephrotropic; gene therapy; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-OCT-2001
Rosen
                                           (HUMA-) HUMAN
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CA,
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Barash
                                                                                                                                                                                                                                                                                  2000US-0246525.
2000US-0246526.
2000US-0246528.
2000US-0249210.
2000US-0249211.
2000US-0249214.
2000US-0249265.
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2000US-0239937.
2000US-0246476.
2000US-0246477.
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2000US-0234997
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2000US-0250391
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                                           GENOME
SC,
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                                           SCI INC
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                              Sulphate Permease; sulphate assimilation protein; wheat; probe; mapping; marker; plant breeding; chimeric gene; transgenic plant; antibody; screen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel plasma membrane associated proteins useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancer, immune response and neuronal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AAM42347-AAM42415) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel genes (AAI62752-AAI62961) and proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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                                                                                                              WO200004154-A2
                                                                                                                                               Triticum aestivum
                                                                                                                                                                                                                                                Wheat sulphate permease-2.
                                                                                                                                                                                                                                                                                 23-MAY-2000
                                                                                                                                                                                                                                                                                                                AAY44945;
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                                                                               27-JAN-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 AERLHVSATLACLTAIIQMGLGFMQFGFVAIYLSESFIRGFMTAAGLQILISVLKYIFGL 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 sffplltyffxggvhqmvpgtfavisilvgniclqlapeskfqvfnnatnesyvdtaame 68
                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFFPLLTYFFLGGVHOMVPGTFAVISILVGNICLQLAPESKFQVFNNATNESYVDTAAME 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-476225/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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91.0%;
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                                                                                                                                                                                                                                                                                                                                                   593
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Pred. No. 8.9e-53;
3; Mismatches 8
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14-JUL-1998; 13-JUL-1999;

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present amino acid sequence is the wheat sulphate permease, a sulphate assimilation protein. This sequence is obtained from wlm4 library, clone wlm4.pk0016.all, derived from wheat seedlings, 4 hours after inoculation with E. graminis. It has 73% sequence identity to Arabidopsis thaliana sulphate permease (gi 2626753). This sequence is used as a probe to isolate other plant sulphate assimilation proteins, for genetic and physical mapping of related genes and as markers of traits linked to the gene. This is useful for plant breeding and to construct chimeric genes, used to create transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid fragments encoding sulfate assimilation proteins in plants and seeds useful as probes for isolating cDNAs and genes encoding homologous proteins, in producing transgenic plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 isolate cDNA clones
snrgpdvg--
                               NNQTPANGTSVSYITFSPDSSSPAQSEPPASAEAPGEPSDMLASVPPFVTFHTLILDMSG
                                                                              YLWRKSKLDCCIWVVSFLSSFFLSLPYGVAVGVAFSVLVVVFQTQFRNGYALAQVMDTDI
                                                                                                                                                                                          savnhesgaktglsgiimgiiicsallfmtplftdipqcalaaiv-isavtglvdyeeai
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                                                              yrntlqypeaytyngivvvrvdapiyfanisyikdrlreyelkl-
                                                                                                                        flwgidkkdfflwamtftttltfgieigvlvgvgfslafvihesanphiavlgrlpgttv\\
                                                                                                                                                                                                                          TLAVDGAGGKSQVASLCVSLVVMITMLVLGIYLYPLPKSVLGALIAVNLKNSLKQLTDPY
                                                                                                                                                                                                                                                                                      IGTAFSLAIVSYVINLAMGRTLANKHGYDVDSNQEMIALGCSNFFGSFFKIHVICCALSV
                                                                                                                                                                                                                                                                                                                                                      RYMHKIRFPIPTEMIVVVVATAISGGCKMPKKYHMQIVGEIQRGFPT-PVSPVVSQWKDM
                                                                                                                                                                                                                                                                                                                                                                                    pliesiiagidqfswppfvmgsaflvillimkklgktn-kklrflrasgpltavv----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LACLTAIIQMGLGFMQFGFVAIYLSESFIRGFMTAAGLQILISVLKYIFGLT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   593
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Pred. No. 3.2e-49;
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fewapkytfq-flkadliagitiaslaipqgisyaklanlppilglyssfippliyammg

Matches

Similarity

14.68;

Score 566; DB 21; Pred. No. 4.1e-48; 8; Mismatches 293;

Length

Indels 132;

Gaps

19;

Conservative

128;

4

PRPRYVVDRAAYSL--TLFDDEFEKKDRTYPVGEKLRNAFRCSSAKIKAVVFGL---LPV 58

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Query Match
Best Local S
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                                                                                                                                                                                                                                                          useful for plant breeding and to construct chimeric genes, used to create transgenic plants with altered levels of sulphate permease. The sulphate permease peptides are useful for producing antibodies, that are used to screen and isolate cDNA clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid fragments encoding sulfate assimilation proteins in plants and seeds useful as probes for isolating cDNAs and genes encoding homologous proteins, in producing transgenic plants -  \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} 
                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        579
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plant;
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RESULT 11
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XX AAY449
AC AAY449
XX Sulpha
KW Sulpha
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COS Zea ma
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                                                                             GIKIITYCSPLYFANSEIFRQKVIAKTVSLQELQQDFENAPPTDPNNNQTPANGTSVSYI
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               tffpddplrqfrgqpnrtkl--
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                                                   14.2%;
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                                           Score 549; DB 21;
Pred. No. 1.9e-46;
0; Mismatches 251;
             -iraaqy-ifpilqwcpeysf-sllksdvvs 72
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Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
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promoter;
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RESULT J
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                                                                                                                                                                  AAG31620 standard; Protein;
                                                 Arabidopsis thaliana
                                                                                                         Arabidopsis thaliana protein fragment
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                                                                                                                                                                                                                                                         gnidtsgismmveikkvidrralklvlsnpkgevvkkltrskfigd-hlgkewmfltvge
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                                                                            genetic
                                                                            signal transduction pathway; metabolic
netic mapping; gene expression control;
                                                                                                          SEQ ID NO:
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                                                                            promoter;
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19-JUL-1999; 19-JUL-1999;

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es 274; Indels 141;
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Search completed: April 26, 2002, 09:05:16 Job time: 207 sec

